

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCA**ATG**GCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCAC TGCGGTATCCTTCTTG CAGTTGGCATT TGGGGCAAGGTGAGCCTGGAGAATTA
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTGGTCGAACTGGTCGCTGCCATCGTAGG
ATTTGTTTT CAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGTTGTGGTGT CACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAGGATT
TCCTAAGAGTTGCTGTAAACTTGAAGATTGACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTTCCCTTTGGAGTTGCTTGCTTCCAAC TGATTGGAATCTTTCTCGCCTACTGCCWCCTCTCG
TGCCATAACAAATAACCAGTATGAGATAGTG**TAA**CCCAATGTATCTGTGGGCCATTCTCTCT
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAAAC TACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATT CATGTTAGATCG
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

FIGURE 2

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><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSLIENYFSLLEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNTNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGGVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
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Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTACAAA
 GGAGTCGCGCCGCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT
 GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
 GCCGGGGTAGGCTCTGAAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTCTAGAAGAGGGT
 GTTCCCTCTTTTCGGGGTCTCTACCAGAAGAGGTTCTTGGGGTCGCCCTTCTGAGGAGGCT
 GCGGCTAACAGGGCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTG
 GGAATAAGCTCTGCAACTTTCTTTGGCATTAGTTGTTAAAAACAAATAGGATGCAAATTCC
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAAAGTAAAACTACCTAAATGATCGTCTTTG
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
 CACATAGCCCCTTCTTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
 CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCCGCCACCAAGGAGGGGC
 CGAGGACCTCATGAGCCAAGGAGAAAGAAAACAAAATGTGGATGGGCTAGTGTGGACACACT
 GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
 GAAAAGTGTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
 TGATAAGATTTGATGTTTTTGCTTGTGCTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
 TGTAGCAGAAAACAGGATAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPFRGRGPHEPRKKQNV DGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTCAGCCCATTGCGC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTCCTAACGACTG
CAAGATGGAGGAAGGCGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCGTTGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTCCGAAGC
CTTCCCCGACATACTTCGGACTAGTGCAGAGCAAACCTCTCCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTACAGCATGCTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCCTGAGCCTTACGCTGGCCACTGTCAAC
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GCGAGGCCTGGGTGGGAGGTACCAGGCAGCCACCAGGGTCCCCTGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
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AAAAAAAAAAAA

FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGNNLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFFPYFHISM
GCAFINLCLILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFRRYHGLSSLCNLGCVLNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

FIGURE 8

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
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ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEGKLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVS SVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCEIPEGLFKTNLADPVKIEKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCC**AT**GGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCTGACGCCGCCAGTGGGCGGGGCCCTTGGGCGCTCGCCACCACT
 GTAGTCATGTACCCACCGCCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACCGTGAG
 CTTTGGCGGAGAGCTATGACAACAGCAAGAGTTGGCGCGCGCTGCTGCTGGAGGAATGGA
 AGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTTCTCCTTGCCCTTTTCTGCTTTTCTGT
 GGACTCCTCTTACATCAACTTGGCTGACCATTGGAAGCTCTGGCTTTTAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAACACCAGCAATCCACCCCTCTTACCAG
 CTCCTCAGAAGGCGGACACCGACCCCTGAGAACTTACCTGAGATTTCGTACAGAAGACACAA
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGCCTGAAGGA
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 ATCCGCGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG
 CTCCCTTCAAGAAGAGCAGAAGTGCCCAACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG
 CACACCAGTGCATCTGAACATTCGCCAGAAGGGCGTGATTGACGCTCTTCTGCATGCATGGA
 AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT
 GAGTGGTTTGGCTCGGTCTCACACTGATCGACGCGCTGGACACCATTGGGATCTTGGGTCT
 GAGGAAGAATTTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTTGAAAAGGAGC
 TGGACGTCAACCTGTTTGGAGCAGCATCCGCATCTGGGGGGGCTCCTGAGTGCTTACCAC
 CTGCTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC
 CTTTCAGAACACCAATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCAC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGG
 GAGCTCTCCCGCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA
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 GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGGCCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA
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 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGGCCAGGA
 GCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
 TGCATTTCAACCTTTACCCACAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGCAGG
 CACAACCTGCTCGGCGCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGGCTGCCAGGGA
 CCGCAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCC
 CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCGAGCCTAGGGAC
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGTCTTCTCCGATGA
 CCCAAACCTGCTCAGCCTGGACGCCCTACGTGTTCAACACCGAAGCCCACCCTCTGCCTATCT
 GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG
 CTGGCTCTGGCATTTTTCCAAGGGGCCACGTAGCACCCGCAACCGCCAAGTGGCCAGGCT
 CTGAACCTGGCTCTGGGCTCTCTCTGCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA
 GGCCGTAGTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCTGCTTCTCT
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 GAGGGGGGCTTCGAGGTGTCCTGGTACTGGGGTGACCGAGTGACAGCCAGGGTGCAGC
 TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA
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 CTGGCCGCCCCGAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGCTCTAGCTCACGGGCCCT
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FIGURE 10

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><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTTPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSTFGESYDN
SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLLFCGLLFYINLADHWKALAFRLIEEEQKMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTLPSSRAEVPTKPPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFESTITRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLTFFVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRNLLRPETVESLFYLYRVGTDRKYQDWG
WEILQSFSRFRTRVPSGGYSSINNVDPPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA

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Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGCCGGCCGGGCTGCGAGCGCCTGCCCATGCGCCGC
CGCCTCTCCGCACG**ATG**TTCCCTCGCGAGGAAAGCGGCGAGCTGCCCTGGGAGGACGGC
AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTGGC
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCTGGCAGTGCTGGT
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCTCTGA
GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACTTCAAGTTCAAC
CGGGCAGCGCTCATCAACGTGGGCTTCCCTGGAGAGCAGCAACAGCAGACTACATTGCCAT
GCACGACGTTACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
CCTTCCACGTGGCTCCCCGGAGCTCCACCTCTCTACCACTACAAGACCTATGTGCGCGGC
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
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AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC
CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC
AGC**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
CAAGGCCTCAGGTCGTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
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FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531

><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

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GQGQETSGPPRACPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFVPHMRRFLSRKKI
RHIIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPFAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYYRIKAGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAAQKEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGTCT
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTCCCCCTTCCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
CCTGTTTCATTAAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGT
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FIGURE 14

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

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MLLLTLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ
PRGEGEKVGDG

Important features:**Signal peptide:**

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGACGGGACAAAG
GAGCATGTCCGCGCCGGGAAGGCCGCTCCCGCGGCCATAAGGCTCCGGTCGCCGCTGG
GCCCGCGCCGCGCTCCTGCCCGCCGGGCTCCGGGGCGGGCCGCTAGGCCAGATGCGCGCCG
CTCGCCCCGAGGCCCGCCGCGCAGC**ATGG**AGCCACCCGAGCGCCGCGGGCGCGCGCA
GCCCGCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGCGCGCG
CGCGCGCGCCGCGCGCTGCCCGCGGGCTGCAAGCAGATGGCGGGCCCCGAGGGGCTGGC
AGGGCGCGGGCGCGCCGAGGGCAAGGTGGTGTGCGACGCTGGAATCTCGCGCAGGTCCCT
GCCCCAGATACTCTGCCAACCCGACGGTCACCCTGATTCTGAGTAACAATAAGATATCCG
AGCTGAAGAATGGCTCATTTTCTGGGTAAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT
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TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAGGATG
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TAAAGCCTGCAGTAGGATTTGTGCACTGCTTTCAGCGCATTTGCTACCTACCGGCTAGCCGGTG
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ACTGGCTTCACGGGGATGACCTGTACCGTGTTCAGAAAAGTGGCAGCCTCTGATCGTACAGG
ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTTAAGT
GCAATGTTTTCAAAATCATTTTTCGAGTCTGGCACTAAAGGTATGTTACATTTCTGCAATCATT
AAGACTATTTACAGT**TAA**AATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA
AAAGATTTTTTTTTGCGAAGATAGGTATTATTGCTTTTGGCTACTGTTTTAAAGAAAACATA
ACGAGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTGCCCTTTGATTCCTTT
CTTCACATAAAAAATATCAGAAATACATTTTATAACTGCAGTGGTATAAATGCAAAATATAC
ATTGTTACATGTGAAAAAATTTTATTGACTTAAAGTTTATTTATTTGTTTTTTTGCTCCT
GATTTTAAAGCAATAAGATGTTTTTCATGGGCCCTAAAGTATCATGAGCCTTTGACATGCG
GCCTGCCAAGCCTAGTGAGAGAAGTCAACCTCTGAGACCAGGTGTTTAAATCAAGCAAGCTGTAT
ATCAAAATTTTTGGCAGAAAACAAATATGTCATATATCTTTTTTAAAAAAGTATTTCA
TTGAAGCAAGCAAAATGAAGACATTTTCTAGTATTTTAAATTTGGTGCTTTAGATATATTT
GACTACACTGTATTGAAGCAAAATAGAGGAGGCACAACCTCCAGCACCCCTAATGAACACCAATT
TTTTTCACTTAGCTTCTGTGGCATGTGTAATTGTATTCTCGGCTTTTTAATCTCACAG
TACTTTATTTCTGTCTTGTCCCTCAATAATATCAAAAACAATATTCAGTCAATTTTAAATGGC
TGCATAATAACTGATCCAACAGGTGTAGGTGTTCTGGTTAGTGTGACACTCAATAAATA
TTGAATGAATGAACGAAAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRGRAQPPLLLPLSLLALLLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSELELAQVLPDPTLPNRTVTLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
 FWGLSSLKRDLDTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLFQT
 EYLLCDCNIIWHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMT
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGCCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLAGITA
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNL
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVMDIASNIMLA
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
 384-390, 403-409, 554-560

FIGURE 17

CGGTGGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCCAAATTCGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA
TCATTGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGAGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 18

MSRSSKVVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

MSRSSKVVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

FIGURE 19

CTGTCGCTCTTTGCTTCAGCCGCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCC
 CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC
 GCTGCCATGCCAAGTGACGGTAACCCGCACCACCATCACAAACCACCACGAGCTCATCTTCGGG
 CCTGGGGTCCCCATGATCGTGGGGTCCCCTCGGGCCCCTGACACAGCCCCCTGGGTCTCCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTTCGCTTCTCCGTGACCCGTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCCCTGCTATGCGGGCCCTCTTCTGCTCTCGGCCCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCTGTCCCACGGCCGTTTCGCGGGACCAAGCATCGCCGCCACCTTCTTCT
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCGGGCCCGGCCCGCGAG
 ATCACTGGCTATATGGCCACCGTACCCGGCTGTGAAGGTGCTGGAGACCTTCGTTGCCTG
 CATCATCTTCGCGTTTCATCAGCGACCCAACTGTACCAGCACCAGCCGGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG
 GAGTGCACCAAGTGCTACCCATCCCCCTTCCCAGCTTCTGTGCGGGCTGGCCCTGCTGTCT
 TGTCTCTCTATGCCACCGCCCTTGTCTCTGGCCCCCTTACCAGTTCGATGAGAAGTATG
 GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGACGCCATGCCTACTACGTGTGT
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGACTCTGCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC
 CGTCCCCCTCTCCAACCTCTTTGTTCTTCTTGCCGAGTTTTCTTTATGGAGTACTTCTTTCC
 TCCGCTTTTCTGTGTTTTCTCTTCTGTCTCCCTCCCTCCACCTTTTTCTTTCCCTTCC
 CAATTCTTGCCTCTAACCACTTCTGGATGCATCTTCTTCTTCCCTTTCTTCTGTGT
 TTCCTTCTGTGTTGTTTTGTGCCCACATCCTGTTTTTACCCTGAGCTGTTTTCTTTTTT
 CTTTTCTTTCTTTTTTTTTTTTTTTTTTAAAGACGGATTCTACTCTGTGGCCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCTCCTGGGTTCAAAGCATTCTCCTCC
 CCCAGCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTT
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGGCTGTGGCTTTCTTATCTGCCTGT
 TTTGCAAGCACCTTCTCTGTGTCTTGGGAGCCCTGAGACTTCTTTCTCTCCTTGCTCCA
 CCCACCTCCAAGGTGCTGAGCTCACATCCACCCCTTGCAGCCGTCCATGCCACAGCCCC
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCCCTTTCT
 CCCAGTGGAGGAAGGTGTGAGTGTACTTCCCCTTAAATTAAAAACATATATATATATAT
 ATTTGGAGGTCAATAATTCCAATGGGCGGGAGGCATTAAGACCCGACCTGGGTCCCTAGG
 CCCCGCTTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTTCATCCCACTATTCT
 CTGTGGTATGAAAAAG

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCSVTLLIILIVELCGLQARFPLSWRNFPI TFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAI AATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQP ALEWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 21

[illegible]

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSLAQVNLSPFSPKVMHDPNYCHPSTSLHLC
 LAWSFTRLHPPLSPGISQVVKDHTKPTAMAQGRVAHLIEWKGWSPSDSPAALSAFSSY
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSLEDGLLGSPARLASQLLGDE
 LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
 QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
 285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTTCCCT
GGCACCCCTCTGCTCAGTGCGACATTGTCACTTAACCCATCTGTTTTCTCTAATGCACGA
CAGATTCCCTTCAGACAGGACAACCTGTGATATTTAGTTCCTGATTGTAATACCTCCTAAG
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
TACAATCTATCTTGCCACATCAAGGATTGTTATTCCTTAAAAAAAACCAATACCAAAG
AAGCCTACAA**ATG**TTGGCCTTAGCCAAAATTTCTGTTGATTTCACGTTGTTTTATTCACTTCT
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT
TTAAAACAATGAAAAATAAACCTATTTCTTTGGAAGTGAAGCAAACCTAAACTCAGATAAA
GAAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCTCCTTTGAATCTACCCAAACA
CAGCCACGGAATAACAGATTTCTCCAGTAACCTCATCAGCAGAGCATTCTTTGGGCAGTCTAA
AACCCACATCTACCATTTCACACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT
TGGAAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
TGCTCTGTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA
ACAGTTCCATTACAGTTAGCATCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
ATAGTGGAAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
TCAAGAAAAACAAGCTCTACAGCCTACCTTAAAAATTCACCAATAATTCAAAAACCTTTTCCAA
ATACGTCAGATCCCCAAAAGAAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGTACTTGTGTGTGAAAAAGGAAAAC
GGATTCAATTTCCCATCGCGCACTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACA
ATGCACCGGAACCTTATGATGTGAGTTTGGGAATTCTAGTACTACAATCCAACCTTTGAAT
GATTGAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCATGGATGACATACC
TCCACTTCGTACTTCTGT**AGAA**CTAACAGCAAAAAGCGTTAAACAGCAAGTGTCATCTA
CATCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT
TTTGTCAAGGAGAATCATAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTTTCTTCTTACAATTTTGGCCATCCTGAGGCATTACTAAGTAGCCTTAATT
TGTATTTTAGTAGTATTTCTTAGTAGAAAAATTTGTGGAATCAGATAAAACTAAAAGATT
TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAATTTATCCACCAAAAAATTTCTAAA
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAAATCAAGATTGCAT
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTCT
TAGTACGTTATAATTTCTAGATCAGCACACATGATCAGCCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT
TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTAACTTGCTTAAATATATCTTAGGCTTCAA
TTATTTGGGTGCCTTAAAAACTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNTPSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNDSA
MP ESEENARDGIPMD DIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACT**ATG**GTGAAAATCGCCTTCAATACCCCTACCGCGTGCAAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTTCATTCACTTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT
 TCATGCCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTCCTCTGATAGTGACCCCTGCGAG
 CAATTATTCACTGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGTCTGGGGAAGTGC
 TATCTGATGCCCCTCAATACTTCTATTGTTATGCCCTCCAAAAAATCTGGTAGAGCTCTTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAAATTTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
 AAGTCTTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGTCTTGGAATAAGAAGTCAGAGATTACAATATGACTTTAA
 CATTAAAGGTTTATGGGATACTCAAGATATTTACTCATGCAATTTACTCTATTGCTTATGCTTT
 AAAAAAGGAAAAAAAAAAAACTACTAACCACCTGCAAGCTCTTGCTCAAATTTAGTTTAAT
 TGGCATTGCTTGTTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTTCTTTGCATTTATAG
 GGTTTAGATTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC
 GTTGTTTTTTTTGTGTTGTTTTTCTTTTCCTTTAAGTAAGCTCTTTATTCATCTTATG
 GTGGAGCAATTTTAAATTTGAAATATTTTAAATTGTTTTTGAACCTTTTGTGTAAATATA
 TCAGATCTCAACATTGTTGGTTTCTTTGTTTTTCAATTTGTACAACCTTCTTGAATTTAGA
 AATTACATCTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
 TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCACAA
 CCCTATAATAAATTTTACTCTATACAAAAAAAAAAAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCM LTLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSPAIIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPKKNLVELFGKLAG
RYLPQTYVVREDLVAVEEIRDVSNLGIIFYQLCNNRKSFR LRRRDLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCCAGAGCAGCCCCGGGCACACGACGGAAGTCTCT
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTGCGCGGAGCACCAGTCTGTACGCC
 AAGGAACTGGTCTTGGGGGCACCATGTTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCTGAAGGCCAGTT
 CCTGGAGGATGTGGCGGGTAGTGGGAGGCCGAGGGCTCGTCGGCTCCTCCCCAGCCTCC
 CGCCACCTTGGACCCCGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAAACCTGGGG
 GGCCCATCACCCCACTTCTGATGGGATAGTGGACTTCTTCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCTGGCCTTTCTGCTGATTCATCGTCTGTGCCCGGTCA
 TCACCCGGCAGAAGCAGAAGGCTCGGCCTATTACCATCGTCTTCCCCAAGAAGAAGTAC
 GTGGACCAGAGTGACCGGGCCGGGGGCCCCGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCCGAGGAAGCCTGGATTCTCCCGGCAGCTCCAGGCCACATCTTGGCCG
 CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACAGGAAGTCCA
 GGGACATGGGGTCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCAG
 GAAGCCCAGGACAGTGGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCACCCCCAG
 TGTCTAAACAGTCTCCCCGGGCTGCCAGCCCTGACTGTGGGGCCCCAAGTGGTCACTCCCC
 GTGTATGAAAAGGCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGGCCTCCCTGTGG
 TGCCAATCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA
 GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
 ACAGCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGTGGGATTACAGGCGTGAGCCACCGTGCCGGGCCAAACTACTTTTTAAACA
 GCTACAGGGTAAATCCTGCAGCACCCTCTGGAAATACTGCTCTTAATTTTCTGAAGG
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAATCCTC
 TCAAGCGCTCTCAAAGCACCCTCGGCTGGGGGTGAGTTTCTCATCCGCTACTGCTGCTGG
 GATCAGGTGAATGAATGGAAGTCTTCTGTCTGGCCTCCAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTTGAGGGGACCTCACCTTGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG
 CCCAGCCTGGAGCAGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG
 TGTCCACAATATTCGTAGTCTCTCGACAGGAGCCTGGGCTCCGTCCTGCTTTAGGAGGCT
 CTGGCAGGAGTCTCTCCCCATCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCAATAAACCTTTATTCCGGCTGAAAAAAAAA
 AAAGA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPWPAL
SPTSMGPQPTTLGGPSPTNFDGIVDFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLALLCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWQGQGGNGGPPNFGTNTQGAVAQPGYGSVVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQS GSSSGSGSNGDNNNGSSSSGSSSSGSSSSGSSSGSSSGSSSGNSGSGSRGDSGSESSW
GSSTGSSSGNHGSGGGNGHKGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
GGSGDNYRQGSSSWGSGGGDAVGGVNTVNSETSPGMFNFTDFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCGGGCGGTGCTCACC
 TGCCCTGGGTGGTGAGTTCTCTCCTTTGCTGACCATTGTGTCCCTTGCTGGAATATTACCGGGACATCTTCA
 CTCTCCGTGCTGGCTCGCCGAGCTGTGGTGTGTCGAGGAGTGAAGGGAAATGTTGTTTCTTCCGTAACAAAG
 TGCTGCTACTTGTCTCTCTGGGCTGGCTTTTCCAGATTCCACAGTCCCTGAGGACTTGTCTTTCTGGAAGAGG
 GTCCTCATATGCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCGCCCTGTGGTGAGCCAGC
 AGCTGTCTTACACCTGCTGCCCTACATCGGAGAGTCCGGAACCTGCTCGCTTCTGGGTGTGAGGACATGATG
 GACGGAGTGGGGGCTTCATGAGGAAATACCCCCACCACTACCACAGCTGGGAGGCCAGCCTTCCAGACCA
 GCCAGGGGCTCGAGGCACAGCTCGCCAGGCTTTTCCACAACCAGCCGCTCCTTGCGCCGAGCCGTAGAGT
 TCGTGGCGAGAAAGATTGGATCAAACTGTGTCAAACTATCAAGGCTACACTGGTGGCAGATCTGTTGCCGCCAGG
 CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGACCAGCCCCAGCTGTTGGAGATCT
 TGTGTTCCAGCTGTGCCCTCAGCGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTGTGTCAAAGGAAGAGCCCTG
 GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGCAGCCGTTCTGAGCAGTCAGAGAAACATTGCTGTGGGGC
 TTGTCAACAGAGAAAGCCTGTGCTTGGCTGTGAGCAACATACAGCACTGATCAGGAGGGAGGTGAAGACGACGAG
 TGAGTGCACACACTTCGAGCCCGAGGCTCTGAACCTGTGTCGCCGGGGAGCGGAGGGGCTGCTCCCGCGCTTGA
 GTGCTCTCCTTGGCCGTGGGGCCACGGGACCTTGACGAGGGAGTCTCCCCAGAGCATCTGGAACAGCTCCTAGGC
 CAGCTGGGCGACAGCTGCGGTGCGCCAGTTCTGTGCCACCTGTGTGAGCAGCATCTGGCAAGTGTCTGTGTG
 GAGTTAGCTTCCCTCCTGTTGAGATCAAAATCTCTATCCTAGGGCCCGCGGACAGTACAGGCTGGAGAGAGGG
 CAGGCTCGAAGGCTTCTGCACATGTCTGCTTTCCCTGTGGAAGGAAGACTTTCAGGGGGCGGTTCGCTGCAGCTG
 CTCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAAAGGCCAAGGGAGTGGGACTTGTGCTGATTTCTGTCTA
 CGGGAGCTGGTGGAGAGGGTCTGATGGGAGGATGGAGATAGAGGCTGCTGGGCAGCCTCCACAGGCCAG
 TGGCAGGGGACTTGTCTGAAGAAATAGCAACACTGTCTAATCTGTTTCTAGCCGAGCCCCACCTGCCAGAACCC
 CAGCTAAGAGCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC
 CTGCTTTGGGCTTGACACAGAACCTTGACCCCCGCTCAGGAGGAGGCCCAAGTGCCTACTGAGACACCTCAG
 TGGTTGGGGTGTAGCTGGGTCTACAGTCAAGCTTCTGTCTAAGGGTGTCACTGCTGGCATCCACACCGCGA
 ATCCTAGAGAGGAGAGGTGGCTGATTTGGGATATGGCAGAAAGTCCAGAGATCTCTGGATGCTGAAG
 GAGGTGGTGTGTTTATCTCTTGGATATAAATGAAATGAGGTGTGTGGGCTTGTCAACACAGAAATCAAGCT
 CATTTGCTATCCAGCATCTCTTAAACCTTTGTAGTCTTGAATTCATGACAGAGGCAATGACTCTGCTTAAC
 TTATGAAGAAAGTTAAACATGAATCTTGGAGTCTACATTTCTTATCACAGGAGCTGGACTGCCATCTCCTT
 ATAAATGCTTAACACAGGCGGGCTTGTGGCTCATGCTGTAATCCAGCAGCTTTGAGAGGCTGAGGTCCGGC
 GACTGCCTGAGGTGAGGAATTAAGACAGCCTGGCCAACATGGCAAAACCCATCTCTACTAAAAATAAAAAA
 TTATTAGCTGGGCATGGTGGTGTGTGCCTGTAATCCAGCTACTCAGGAGGATGAGGCGAGGAGACTGCTTGAAC
 CTGGAGGTGGAGGTTGCAGTGAGCGAGGTGCGACCACTGCACTCCAGTCTGGGTAAACAGAGCGAGACTTCTAG
 AAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCCCTGTACTTTCAGCCCCGT
 TGCAGGTAGTAACCTCTTGAGACTCTCCCTGACCAGGGACCAAGCACAGGGCATTTAGAGCTTTTGAATAAA
 CTGGTTTTCTTTAAAAAAGGGCTTTTATTAATAATCTCCACACAGTGGCTCTGCAATCTGCCACAGCTC
 TGGGCGCTGTCTGTAGGGAAGGCGCTGTTTTCCCTGAGGCGGGGCTGGGCTGTCCATGGGTCCGCGGAGCTG
 GCGCTGTGCGGCTGGGCTGGGCTGTGCTAGCTGCTTCTGCGGGCACAGAGCTGCGGGGTTCGGGGGACCGGG
 AGCTTAAGAGCAGGCTCTGGTCAGGGGTGGAGGCTGTCTTAAACGACACCTGAGGTGCTCTGAGATGCTG
 GGTCCACCTGAGTGGCAGGGGAGCAGCTGTGGCCGCTGCTCCTTCYTAGGCCAGCTCTGGGGAACATAGCTC
 GGGCCCTTTTGGCAAGACCGAGGATGGGTGGGTGGGTGGGGGATCATGGGAATGGCTGAGGAGCTACGTGT
 GAAGAGGGCGCGGTTGTGGCTGCAGCGGCTGGAGGCGCTTCTCCTGAGCCTCAGTTTCCCTTCCGCTCTA
 ATGAGAAACATGCGGTCTGCGGTCTCAGGGCTATTAGGACTTGCCCTCAGGAAGTGGCTTGAAGGAGCTCAT
 GTTATTTCACAACTGTCTGCGACGTTGGCTGGGACGCTCATGGAATGGCCCATGTCCCTCTGCTGCGGTGAC
 GTCGCGGTGCGGAGTGGCAGGCGGAGGCGGGGCCAGACGTGCGCTGGGGGTGAGGGGAGGCGCCCGGAGGG
 CCTCAGAGGAAGTTGGGCTCCCCACCAACAGGAGGGCGGGCTCCCCGCGCGCGCGCCACACCGTCCAGG
 GCGCGGTAGCAAAAGTGAAGTGTGGCTGCTGCGCAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
 TCGTCCGCGAGCTGGAAGCAGCGCCGTCCACCAGCAGCAACAGCGGTGCGCCT

FIGURE 32

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAP EHG L D N A P V V D Q Q L L Y T C
C P Y I G E L R K L L A S W V S G S S G R S G G F M R K I P T T T T S L G A Q P S Q T S Q G L Q A Q L A Q A F F H N Q P P
S L R R T V E F V A E R I G S N C V K H I K A T L V A D L V R Q A E S L L Q E Q L V T Q G E E G D P A Q L L E I L C S Q L
C P H G A Q A L A L G R E F C Q R K S P G A V R A L L P E E T P A A V L S S A E N I A V G L A T E K A C A W L S A N I T A L
I R R E V K A A V S R T L R A Q G P E P A A R G E R R G C S R A

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTTGCGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
 AAGACTCTCTGCTTTTGGCCACAGCAGTTCCTGTCAGTTCCTTGAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**
 AGTAGCAACAAGAGCAGCGCTCAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCTAGCAGGCTATGTCCCCATTCTCGGC
 AACAAGACACTGCCCTCTCGGTGCCACCAGTGTGATTGTGTCAGCAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
 CCACCCTGGCTACTCAGCTGATGTGGGCAACAAGACCCTACCGCGTCGTGGCCCATTC
 AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT
 CATCTTCTGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCCTGTGATCC
 AGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCGGCCGCATGCGG
 CAATTTGACGACCTCTTCCGGGTGAGACGGGCAAGGACAGGAGAAGTCTCATTCGTGGTT
 GAGCACAGGCTGGTTTACCATTGGTGTATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG
 GCATGGTCCCCCAACTACTGTCAGCCAGCGGGCCCGCCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCAAGGGCCGGACGAATGTGTCACTACATCCAGAATGAGCACAGTCGCAAGGG
 CAACCACCACCGCTTCATCACCGAGAAAAGGCTCTTCTCATCTGTGGGCCAGCTGTATGGCA
 TCACCTTCTCCACCCCTCCTGGACC**TAG**GGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
 AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
 TGGGGAATCTGTTGGCGAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTCTGTAGTCAATCTG
 AGGCTAAGGACATGTCCTTTCCCATGAGGCCTTGTTTCAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCACCTCTGCTGGGATAATGGGGTCTGTGCCAAGGAGCTGGGAACCTTGGTGTG
 CCCCCTCAATTTCCAGCACCAAGAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAAATTTGTGGGTGTGTGGAGTTGTGGGGGCGGTGGGAGAGTCCGAGAGGCTGGGA
 GGCTGGCATCCAGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCTTCCCCCTCTCTGGG
 CACCCTTCTGCCCACACAGTTTCCAGTGCAGGAGTCTGAGACCTTTCCACCTCCCCACAA
 GTGCCCTCGGGTCTGTCTCCCGCTCTGGACCTCCAGCCACTATCCCTTGTGGAAGGCT
 CAGCTCTTTGGGGGTCTGGGGTGACCTCCCACCTCCTGGAAACTTTAGGGTATTTTTGCG
 GCAAACCTCCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAACCTTAAGCTGTTTTCT
 TAGCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCCTCTTTTCTGCCCT
 CTAGCAGGGAGGTTTTCCAACCTGTTGGAGCGCCTTGGGGCTGCCCTTTGTCTGGAGTCA
 CTGGGGGCTTCCGAGGGTCTCCCTCGACCCTCTGTCTGCTCTGGGATGGCTGTGCGGAGCTGT
 ATCACTGGGTCTGTCCCTGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCCTCAGTGG
 GGTGTGTTTGTCTCTGTCTCTGTGGAGCCTTGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG
 GGGCGGTGACTGCCCCAGACTTGGTTTTGTAAATGATTTGTACAGGAATAAACACACCTACGC
 TCCGGAAA

FIGURE 34

MSSNKEQRSADFVILFALITILLYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
GNKTLPSRCHQCIVVSSSSHLGLGFEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
SSVFRVLRRPQEFVNRTPETVFIFWGGPPSKMQKPQGS LVRVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDRKSHSWLSTGWFTMVI AVELCDHVHVYGMVPPNYCSQRPR LQRMPYH
YYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTTCCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAAAGGAACTCAGCGGACCGGGAGCGACGCAGCTT
 GAGGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGTTGTCAGGGGGCTGG
 GGCAAAAGGTGAAGAGTTTTCAGAAACAAGCTTCTGGAACCCATGACCCATGAAGTCTTGTGCAGATTATACCGT
 CTGAGGGTAGCAGCTCGAAACTAGAAAGAGTGGAGTGTGCCAGGGACCGCAGTATCTCTTGTGTGACCTTGGC
 GGCTATGGGAGCTTGGCTTCAGAGCTTTGTGATACACCACTGCTCGTGGGACGATGACGGCGTGGAGAGGAAT
 AGGCGTGAAGTTCACACTGGCTTGGCTCCTCTAGCCACAGCAGGCTGCTTGTCTGACTTGAACAGAGTCCCTCAG
 GTCAACGCTCAGCCTGGCTCCACCGTCCAGAAAGCCGGAGGCACTGTGATCTTGGGCTGGCTGGTGGAACTCCCA
 AGGATGAATGTAACTTGGCGCTCGAATGGAAGGAGCTGAATGGCTCGGATGATCTGTGGTGTCTCTCATCTCACC
 CACGGGAAGTCTCGTCATCTGCCCTTAACAACACACTGTGGGACGATACCAAGTGTGTGGCCGGATGCCGTGG
 GGGGCTGTGGCCAGCGTGGCCAGCACTGTGACACTAGCCAACTCTCCAGGACTTCAAGTTAGATGTGCAGCACGTG
 ATTGAAGTGGATGAGGGAAACACAGCAGTCAATTGGCTGCCACTGCCGTGAGAGCCACCCAAAGCCAGTCCGG
 TACAGCGTCAAAACAGAGTGGCTGGAGGCTCCAGAGGTAACTACTGATCATGCCCTCAGGGAACCTCCAGATT
 GTGAATGCCAGCCAGGAGGACGAGGCGATGTACAAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAACACC
 TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCAGAGGGC
 CAACCATCATCGTCACCAAAGGCCAGAGTCTCATTTGGAGTGTGTGGCCAGTGGAACTCCACCCCCACGGGTC
 ACCTGGGCCAAGGTGGGTCCAGTGTCAACCGGCTACAACAAGACGGCTTCTGTGTGAGCACTCTCTCATCGAC
 ACCACAGCAGGAGGAGTACAGGCACCTACCGTGCATGGCCGACATGGGTTGGGACGCCGGGGCAGGGTCT
 ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTACCATTGAGAGTATCCGAGCTGTCTATCCCTGGCC
 CAGAGTGGCAAGCTTACCTGTGAGGTGCGTGGGAACCCCGCCCTCCGTGTGTGGTGTGGAATGCTGTGGCC
 CTCTATCTCCAGCCAGCGCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGTGTCAGCATGGGGCTGAGGACGAGGG
 GTCTACAGTGCATGGCCGAGGACGAGTGGGAGCGCCATGCCGTAGTGCAGCTGGGGACCTCCAGGCCAAAGC
 ATTAACCCCAAGCTTGGGAGGATGCTGAGCTGGCTACCTGGCACACCTCTGTATCACCTTCCAACTCGGCAAC
 CTTGACGAGATGCTGAGGCGCTCGGCCTCCCGAGCCCAACCGCTGAGTGGGGCTGCTTCCCGAAGTGT
 CCAGGAGAGAAGGGGCGAGGGGGCTCCCGCGAGGCTCCCATCATCTCCAGCTCGCCCGCCACCTCCAGAGACAG
 TCTATATGAAGTGTGTGGCGGCTCGGCATGAGGTCAGTGGCGGGGGCCAACTCTCTACTATGTGTGTAACAC
 CGCAAGCAGGTCAACAATTTCTCTGACGATTGGACCATCTCTGGGATTCAGCACAACAGCAGCCGCTGACCCCT
 ACCAGCTTGACCCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACCTGTGGGGAGAGGGCGACAGCC
 ATGGTCACCTCCGAAGTGGACGGCGGCCCAACCCGAGATCATGGCCAGCAAGAGCAGCAGATCCAGAGAGAC
 GAGCCTGGAGCCAGTCCCGAGAGCAGCAGCCAGACCCAGGGCCGCTCTCCCGCCAGAAAGCTCCCGACAGG
 CCCACCATCTCCACGGCCCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCGTGGGAATGTTGGTTCCTCAATC
 CAGTCCCTTCGTGTGGAGTACAGAAGCTAAGAAAGTGGGAGACTGGATTGTGGCCACACGCGCATCCCCCA
 TCGCGGCTGTCCGTGGAGTACCGGCTAGAGAAAGSCACCTCTACAAGTTTCCAGTCTCCGGCTGTGAACATG
 CTGGGGRAGAGCGGCGCCGCTCTCGGCCCTACGTGTGTGGCTACAGCGCTCGCGTGTACGAGAGG
 CCGCTGGCAGTCTCTATACCTCTCAGCATCGGCTCAATGAGACCACTCATGTCTCAAGTGTGATGTACATC
 CCAGCACTAACAACAACCAACCTCATGGCTTTTATATCTATTATGACCCACAGACAGTGAACATGATAT
 GAGTACAAGAAGATATGGTGAAGGAGACAACTACTGGCATCTACGACCCCTGAGCAGGACCTCTCCATC
 GACATTAAGATGCAGTCTTCAATGAAGGAGGGAGAGCAGTTCAGCAACCTGTATGATGTGTGAGACCAAGCT
 CGGAAGTCTTCTGGCGAGCCTGTGCAGCTGCCACCCCAACTCTGGCCGCCACACAGCCGCCCTTCTGAACAC
 ATAGAGCGGCCGCTGGGCACTGGGCGCATGTGGCTCGCTCCAGCGACTGCCCTATGTATGTGTGGGTGCTC
 CTGGGCTCATGTTCTCATCATCTCTACCTTCTATCCCTCTGCTTGTGGAGGGCTGTGTAAAGCAAAACAT
 ACAACAGACCTGGGTTTTCTCGAAGTGGCTTCCACCTCTCTGCCGTTATCATTTGGTGCCATTGGGAGGACTC
 CCAGGCGCCAGGCGAGTGGACAGCCTTACTCATGTGGCATCAGTGGACGGGCTGTGCTAATGGATCCACATG
 AATAGGGGCTGCCCTCGGCTGCAGTGGGCTACCCGGGCAATGAAGCCCGAGCAGCATGCCAGGCGAGCTTCAG
 CAGCAGAGTGCACCCAGCAGCTGCTGAGGACAGCCATCTTGGCAATGGATAGTACCCCAAGTCCACAGATG
 CAGAGGGGTCCCAAGTGTAGCCCGGACGAGGGCTTCTTCTTATACACACTGCCCGACGATCCACTCCACAGCTG
 CTCGACGCCCATCAGCACTGCTGCCAACGCCAGGAGCAGCTGTGCTGTGGGCTCAGGGGTGAGGAGGCC
 CCCGAGAGTCTGTCTGGAAGAGCAGTGTGGACCTCCATTTTCACTCAGGCGCCCATGCTGTGTGGGCTGTGTG
 CCAGTGTGAAGAGTGGACAGTCTCTGACTCTGCGCAAGTGAAGGAGAGCTGTGTGCCAGCCCGTATGGG
 GCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCGGGGCACTGTGTGCTGTGTCTTTGAAACACCACT
 CTCACAACTTTAGGTCAGAGTGTATATCCAGAAAGACTATATATTTTCTTATATATGTTTAAAAAAGAGAA
 AGAGACAGAGAAATTTGGTATTTATTTTCTATATAGCCATATTTATATTTATGCACTGTGAATAAATGTA
 TATGTTTATATATTTCTGGAGAGACATAAGGAGTCTTACCCGTTGAGGTTGGAGGGAAATAAAGGAAGCTGCCA
 CCTAACCGAGAGTCAACCAGGAAGAGCACCGCACAGGCTGGCGCGGAGACAGACTCTAACCCTGGGCGCTGTGAGT
 GCGAGGAGGCTGCAGGAGGCCACAGATAAGCTGGCAGAGGAGGATCCAGGACATGTTCTATCAGAGCA
 TGAGGGAACAGCAGAGGGGCGACGCTATCACAGCTGGAGACACCCACAGATGGCTGGATCCGCTGCTACGGAA
 ACATTTTCTAAGATGCCATGAGAACAGCAAGATGTGTACAGCATATGAGCATTAATAAAACCTTCCAGAT
 CAATAATCCGTGGCAACATATCTGTAAAAACAACACTGTAACTCTAATAAATGTTTAGTCTTCCCTGTAAAA

FIGURE 36

MLRGTMATAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQVPASTVQKPGGTIVLGCVVEPP
 RMNVTWRLNGKELNGSDDALGLVLI THGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQ
 IVNASQDEDEGMYKCAAYNPVTQEVKTS GSSDRLRVRRSTAEAAARI IYPPEAQTI IIVTKGQSL
 ILECVASGI PPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELS QLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCAENEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMRLRGQPALPRPPTSVGFASPKCPGKKGQGAPEAPI ILS SPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFR TGRRPKPEIMASKEQQIQRDDPGASQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRGNGGFFIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRV
 RALNMLGESEPSAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMYIPASNNNT
 PIHGFYIYYRPTSDSDNDSDYKKDMVEGDKYWHSISHLQPETS YDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL
 IIVTFIPFCLWRAW SKQHTTDLGFPR SALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCP SAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDP PFHSG
 PPCCGLGLVPVEEVDSPDCSQVSGGDWCPQHFPVGAYVGQEPGMQLSPGFLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCATTGTGCGCCTCTGCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCGCGCAAC**ATG**CAGCCACGGGCCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGGAGACACGCCGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC
 AGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG
 CACCCCCAAAACCTTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCTTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTATTACCGCATGTGTGCCCTCCTACTCTGAACTCGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
 ACCTGACACTTACCTTACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTTCAGACAC
 CACATGTACACCAACGTGAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTGTCTATGCATCGGACACCTTGATAAGAAGGGTCTTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATTGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAATATGACGGGACT
 GGCCGGTTCCCTCAGGGGTGGAGGATGTGTCCACATACCCAGTCTGTAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTCGTGGAACCTGCTGCGGGTCT
 TCAGACAAGTGGAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCTGCCACTCCACCTCGTGCCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCTGGAGGTCTCAAATGCCT
 CCCCATACCTTGTTCCAGGCCTTGTGGTGTGCCACCATCCCAACCTTACCCAGTGGCTC
 TGCT**GAC**ACAGTCGGTCCCCGCGAGAGGTCACTGTGGCAAAGCCTCACAAGCCCCCTCTCCT
 AGTTCATTCAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELV TSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNKGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVVREESRAQSPVEAEFPYGLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVFPWRSSNASPYLVPGLVAAATIPFTTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGCTGGTGCCCCAGCTGAAGCCAACAA
 GAGTTCGAAGATATCCGGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
 TTTACAACCAGAAATGTATCCAGAAAGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTCATCATTTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
 ACATGGCCTTCCTGATGCTGGTGGACCCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCAACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAAACACAGTCTTGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC
 AAGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCT**TAGAT**TGGGCTGG
 TGTGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCTCCTT
 CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCCTTGAAGATAAAAGCTGGGTCTTCA
 GGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTACGATGTGTTCTTTCTGCAGTG
 GTTCTTATCACCCTCCCTCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCCTGGA
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
 CTGCTGCCGTTCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC
 CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCTGTACTTGGGTGCTCTTGTCCCTGAACCTCGTTGTACCAGTGCATGGA
 GAGAAAATTTTGCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAAATTG
 TTTTATTTCTCTCA

FIGURE 40

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGHDEAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGCGGTGAGACTGAGTTCATAGGGTCTGGGTCCCCGA
 ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGCAGCCCAAGTGAGGGGGCCCGTGTGGGGTCTCC
 TCCCTTTGCAATTCACCCCTCCGGGCTTTGCGTCTTCTGGGGACCCCTCGCCGGGAGATGCGCCGGTGTATG
 CGGAGCAAGGATTCCTCTGCTGCTGCTCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCAGAGTCCGGCAGT
 TCGCGGGCCAACTCAACTCCATCAAGTCCCTCTGCGGGGGGAGACGCTTGGTGGCCGCCAATCGATCTGCG
 GGCATGTACCAAGGACTGGCATTCGGCGCGAGTAAGAAGGGCAAAAACCTGGGCGAGGCCTACCTCTGTAGCAGT
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCACCAAGGATCATCGGCTGCATGGTGTCTCGGAGA
 AAAAAAGAACGCGTCCACCCGAGATGTGCTGCCCGAGTACCCGTCGAATTAAGGCATCTGTATCCCAGTT
 ACTGAAAGCATCTTAACCCCTCAGATCCCGGCTCGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC
 TCAAACCATGACTTGGGATGGCAGAACTAGGAAGACCAACACACTAAGATGTACATATAAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTGCTCATTTCTGGACAAAATCTGCAAA
 CCAGTGTCTCCATCAGGGGGAAAGTCTGTACCAAACAAGCAAGAGGGTTCTCATGGGCTGGAATTTTCCAGCGT
 TGGCAGTGTGCGAAGGGCTGTCTTGCAAGATATGGAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG
 TGTGAGAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTAAATGCATTATAG
 CATGGTGGAAATAAGGTTTCAGATGCAGAAGATGGCTAAATAAGAAACGTGATAAGAAATATAGATGATCACAA
 AAAGGGAGAAAGAAACATGAAGTGAATAGATTAGAATGGGTGACAARTGCAGTGCAGCCAGTGTTCCTATTATG
 CAACTGTCTATGTAATAATGTACACATTTTGTGGAATAATGCTATTATTAAGAGACAAGCACAGTGGAAATTC
 ACTGATGAGTAGCATGTGACTTTCCAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCCCTCAGATTGCTGATTGC
 TTATACAAATAACCTACATGCCAGATTTCTATTCACGTTAGAGTTTAAACAAATACTCCTAGATAAAGCTTGTTA
 TACAATAGGTTCTAAATAATAATGCTAAACAAGAAATGAAACATGGAGCATTTGTAATTTACAACAGAAAAAT
 TACCTTTTGATTGTGAACACTACTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT
 TTCCAATAATTTGCAAAATAATGGCCAGTTGTTAGGAAGGCCTTTAGGAAGACAAATAAATAACAACAACACAG
 CCACAATACTTTTTTTCAAAATTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGA CAAAAACAGTTCC
 TTCAGATTCTACGGAATGACAGTATATCTCTCTTATCCTATGTGATTCTCGTCTGAATGCATTATATTTTCCA
 AACTATACCCATAAATGTGACTAGTAAAAACTTACACAGAGCAGAAATTTCAAGATGGC CAAAAAATTTAAA
 GATGTCCAATATATGTGGGAAAAGGCTAACAGAGAGATCATTAATTTCTTAAGATTTGGCCATAACCTATATTTT
 GATAGAAATAGATTGGTAAAAATACATGATTATCATACATACTCTGTGGTAATAGAGACTTAACTGGATCTGTACTG
 CACTGGAAGTAAGCAAGAAATTTGGGAAACTTTTTCTGTTGTCTCAGGTTTGGCAACACATAGATCATATGTCTG
 AGGCACAGTGTGGCTTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCAATGGGATTTGCTAT
 CATATAATTTACTATGCAGATGAATTCAGTGTGAGTCTCTGTGCTGCTACTATCCICAAATTAATTTATTTATAG
 TGCTGAGATGCTCAATAATCTCAATTTTCAGGAGGTTTCAAAAATGTACTCTGAAAGTAGACAGAGTAGTGGAG
 TTTTCAATTCGCCCTCATAAAGCTTCTGACTAGCCAAATGGCATCATCCAATTTTCTTCCCAACCTCTGCAGCATCTG
 CTTTATTTGCCAAGGGCTAGTTTCGGTTTTCTGCAGCCATTCGGGTTAAAAAATATAAGTAGGATAACTTGTAA
 AACCTGCATTTGCTAATCTATAGACACACAGTTTCTAAATCTTTTGAACCACTTTTACTACTTTTTTTTAACTT
 AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAAATAAAGGTTATCTTATAGTCGTGACTTTAACTTTTG
 TAGACCACAAATCACTTTTGTGTTTTCTTTTACTTAAATCCATCTGCAGTCTCAAATTTAAGTCTCCCAGTAG
 AGATTGAGTTTGTGCTGTATATCTATTTAAAAATTTCAACTCCCACATATATTTACTAAGATGATTAAAGACTTA
 CATTTTCTGCACAGGTCTGCAAAAACAAAAATTTAAACTAGTCCATCCAAGAACCAAGTTTGTATAAACAGGT
 TGCTATAAGCTTGTGAATGAAATGGAACATTTCAATCAACATTTTCTATATAACAATTTATATATTTACAAAT
 TTGGTTTTCTGCAATATTTTTCTTATGTCCACCTTTTAAAAATTTATTTTGAAGTAATTTATTTACAGGAAATG
 TTAATGAGATGATTTTCTTATAGCATATTTCTTACAGAAAGCTTTGTAGCAGATATATTTGCAGCTATTGAC
 TTTGTAATTTAGGAAAAATGATAAAGATAAAATCTATTAATTTTTCTCCTCTAAAAACTGAAAAAATAA
 AAAAAAATAAATAAATAA

FIGURE 42

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRCNN
GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25



FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTATCCACCTACCTTGGCCTCCCAA
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCGCCAACATCACGTTTTTAAAAATTGATT
 TCTTCAAATTCATGCGAAATATTTCCCTTCCTTTAACTTCTTATGTGAGAATGAGGAAGGA
 TAGCTGCATTTATTTAGTCAGTTTTCATTGCATAGTAATATTTTCATGTAGTATTTCTAAG
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAAATCTTG
ATGTGTTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTGTTCTTTTATCCCCCT
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTGAGAGCTTGCACCACCAAAATGGCAAACA
 TCACCAGCTCCCAGATTTTGGACCAAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCTACAACCTACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCTCAGTCCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
 CAGTTCCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTGTCTCCT
 CCTGGTTTGGAGTCCTTTCTTCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC
 CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAATATCTCTGTGTCTG
 TCCACCAGCCACAGCCCAACACATCAAACCTGCTAAGCGCGGATACCCCCAGCTTCTAAG
 ATCCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT
 TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCCATCAGCTTGATTTCGAAGTCTTTAAGTGAGCCTTTGAATACA
 TCTTTATCAATGACCAGTGCAGTACAGAATCCACATATACAACCTCCGTCATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTTCATCAGAGTCAGTCCA
 GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTTGTCTATGGCTGGTGCCAACCAACAGAGGAAGAGGATAGCTCACGTGA
 TGTGGAAAACACCAAGTTGGTCAATGGCTCATTGCTTAAAGCAGCCCTTTTGCTTTTTTGT
 TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTCAGCATAACAGTATGCAT
 TTTAAAGATGCTTGGGCCAGGCGGGTGGCTGATGCCCATAAATCCAGTGCTTTGGGGGCC
 AAGGCAGGCAGATTGCCAAGCTCAGGAGTTTGAGACCACCTGGGCAACATGGTGAACTC
 TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTSDWDLKPPTSQSSVLSHLDFKSQPEPSVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPKHIKLAKRRI PPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSESNQIPISLYSKSLSEPLNT
SLSM TSAVNSTYTTSTVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRI PYQSPVSSSESAP
GTIMNGHGGGRSQQTLD SKYSSKLLLSWLVP TKQRKRIAHVMWKT PVGQWLIR

Signal peptide:

amino acids 1-24



FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGCGCTGCCATCCGAATCCTGCT
 TTGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGCGCACCCGCGCTTCTGACCTGCGTGAACCGGGGACAGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGACGCGCCCGGG
 GTCCGCGACGACCGCGCGGACCGCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA
 CGGGCCCTTTTCTGCGGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTTACTGTGGCCTGCACGAACGCCGCTCTTCACCTGACGCTGCCGAACCCACGC
 GGAGCCGCCCGCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCGAGGCCAC
 ACCCACACTGGCGCGCGGCCACAACGTCATCAATGTCGTCCCCGAGAGCCGAGGCCAC
 TTCTTCCAGAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGCTCAC
 TGTCTCCTGGCGCCCGCAGGCGCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGAA
 AGTCAAAGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGTTCCGGAAGGAGAAT
 GCAAATAGGGAGGCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCTTCCAGCGGCTGGTCCCGCTTTCCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCCCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAAAC
 AAAATCCCACTGATGCCCATCATGCCCTCAGACCTTCTGGGCTCTGCCGCTGGGGGCTG
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAACCTGGGGTCAGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGAGGAGTCCCACT
 CCTCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGTCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGACCCCTGCCCTTTCTCTGCCCCATCCCTACCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGAGTGAAGTTGGTTGGGGTGGCCTGTGTTGCCACTCTCAGACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAAATAAGTCCCCATCTGATTTTTAAAAA
 AAAAA

FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWRQPPGVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIE PLEVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEP PPRGSPGN GSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSP LPAKYIDL DKGFRKENCK

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGCGGCGTGGCGCAGCGGCGACATGGCCGTTGTCTCAGAGGACGACTTT
CAGCACAGTTCAAACCTCCACCTACGGAACCAACAAGCAGCTCTCCGAGCTGACCAGGAGGC
ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT
GTGGCACATACATCATCTTCTTACGCTGGGCATTGGCAGTCTACTGCCATGGAACCTCTTT
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA
GGACCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG
TGCCCTCCATGCTGTGCCTGGTGGCCAACTTCTTGCTTGTTCAACAGGGTTGCAGTCCACATC
CGTGCTCTGGCCTCACTGACGGTCATCTTGCCATCTTCATGGTGATAACTGCACTGGTGAA
GGTGGACACTTCTCTCGGACCCGTTGGTTTTTTTGGCGTCAACATTGTCTGCATGGTGATCC
TCAGCGGTGCTCCACTGTCTTACGACGAGCATCTACGGCATGACCGGCTCCTTTCCATG
AGGAACCTCCAAGCACTGATATCAGGAGGAGCCATGGCGGGACGGTCAGCGCCGTGGCCTC
ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTTGACGG
CCACCATCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGCCAGGCTGGAGTATGCC
AGGTACTACATGAGGCCTGTTCTTGCGGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCA
GGACTCCCTCAGTGCCCTTCCGTGGCCTCCAGATTCAATTGATTTCCACACACCCCCCTCTCC
GCCCCATCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGCACCTACGCTCTTCTTTCATCACC
AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
GTGGACCACCAAGTTTTTTCATCCCCCTCACTACCTTCTCTCTGTACAACCTTGTGACCTAT
GTGGCCGGCAGCTCACCGCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCAGGG
TTCGTGCTCCTCCGACCTGCCTCATCCCCCTCTTCTGTGCTCTGTAACCTACCAGCCCCGCGT
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACCTCCTCAGCTCCCTGCTGG
GGCTCAGCAACGGCTACCTCAGCACCTTGGCCCTCCTCTACGGGCCCTAAGATTGTGCCAGG
GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCTCTTTATGTGTGCTTGGGCTTAACACTGGG
CTCAGCCTGCTCTACCCTCCTGGTGACCTCATCTTAGAAGGGAGGACACAAGGACATTGGTG
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAAGGAGGGCTGGGGGCCATGGAGGAAGGCC
TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA
GTGAGCCACGTCCATGCCCATTCCTGCAAGGCAGATATTCAGTCAATATTAACAGAACACT
CCTGAGCAGGTTGAAGAAGAAATAGCACAATCAGGGGTACTCCCTTCACAGCTGATGGTTA
ACATTCCACCTTCTTCTAGCCCTTCAAAGATGCTGCCAGTGTTTCGCCCTAGAGTTATTACA
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCT
GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA
AGTCCCTTGGCATGGTCAGTCTCAGGCCCAAGACTCAAGTGTCACAGACCCCTGTGTTCT
GCGGGTGAACAACCTGCCCACTAACCAGACTGGA AAAACCCAGAAAGATGGGCCTTCCATGAAT
GCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
TTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC
TTTCAGTGTCTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
GTATTCAAAAA

FIGURE 48

MAVVS EDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGLRPEDRFCGTYIIFFSLGI
 GSLLPW NFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
 LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSWTRGFFAVTIVCMVILSGASTVFSSSI
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
 LLLSRLEYARYYMRPVLAAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF
 CVTYVF FITS LIYPAVCTNIESLNKGS GSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
 GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLGLSNGYLSTLAL
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
 305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTCTGCTGTACCAAGAGCTGGAGACACCA
 TCTCCCACCGAGAGTCTATGGCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCTCC
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCTTCGAGAAATGC
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGCGCGGCTGGTGGCCGCCAAGGTGC
 TCAGCGATGCTGGACACAAGGTCACCATCTGGAGGCAGATAACAGGATCGGGGGCCGCATC
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCC
 AGTACGACAAGAACACGCTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
 AAGGTGCCCCGAGAAGCTGGGCTACGCCCTTGCCTCCCCAGGAAAAGGGCCACTCGCCCGAAGA
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG
 CGATGAAGAAGTTTGAAGGCACACGCTCTTGAATATCTTCTCGGGGAGGGGAACCTGAGC
 CGGCCGCGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT
 CGCCGAGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG
 GTGGCTGGGACCTGCTGCCGCGCGCGCTGCTGAGCTCGTGTCCGGGCTTGTGCTGTGAAC
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
 CCCGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGCGAGCGGACCGG
 CGGTGAAGCGCATCACCTTCTCGCCCGCGCTGCCCCGCCACATCGAGGAGCGCTGCGGAGG
 CTGCACTACGTGCCGCCACCAAGGTGTTCTTAAGCTTCCGCAGGCCCTTCTGGCGCGAGGA
 GCACATTGAAGGCGGCCACTCAAACACCGATCGCCCGTCCGCGCATGATTTTCTACCCGCCGC
 CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTCGGACGCGGCGGCAGCGTTCCGC
 GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
 TGTGCTGCGCCAGCTCTGGGACGGCACCGGCGCTCGTCAAGCGTTGGCGGAGGACCAGCACA
 GCCAGGGTGGCTTTGTGGTACAGCCGCGCGCTCTGGCAAACCGAAAAGGATGACTGGACG
 GTCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCCTACCCGCAGCGCTGGGTGGA
 GACGGCGGTCAAGTCGGCGCTGCGCGCCGCATCAAGATCAACAGCCGGAAGGGGCTGCAT
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGAGGGGCATGTGCATGGG
 GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCTCCAGTCCAAGG
 CCAGTTATCTCTCCAAAACGACCCACACGAGGACCTCGCATTAAAGTATTTTCGGA AAAA
 AA

FIGURE 50

MAPLALHLLVLPILLSLVSQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPKLGALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGEFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDLPLALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPARNL
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRPPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLASYTWSDAFAAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVWRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGFPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCGGGCCTTCTGCCTGCAT
 GAGCGCTCTGAAGCCACCCCTGCTCTGGAGGAACCCAGCAGCGAGGGAAGAGGACAGGAGCTCGTGTGGGAGGAA
 GAATCAGAGCGGGGAAGCCGCCATCTACTAGAAGCACTGAGAGATGGCGGCCCTCGCAGGGCTCGAAATTTCT
 GCTGCTGTTCACAAAGATGCTTTTATCTTTAACTTTTGTCTTTCCCACTTCCGACCCCGGCGTGTATCTGCAT
 CCTGACATTTGGAGTGCCTATCTTCTTGGCTGATCACCAGACTCAACCCGTCTTACCTCTTCTGACCTGAA
 CAATCAAGTCTGTGGGAATTGAGGAGGAGCAGCGAAGGGGTTTCCAGAAAGAACATGACCTACAAAGTTGCTG
 CTCTCAGATGCCAAGACTATGTATGAGGTTCCTCAAAGAGGACTCCGCTGTGTCTGACAAATGGGCGCTGCTGGG
 ATATAGAAACCAAACGACCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGGACAGAGTCACTGGGTTCT
 CTGTCTCTTGCAATAAAGTTATAAATCATCACCAGACAGGTTTGTCCGCTATCTTGTCTCAGAATAGGCCAGAGTG
 GATCATCTCCGAATTGGCTTGTACACGTACTCTATGGTAGCTGAACCTCTGTATGACACCTTGGGACCAAGAAGC
 CATCGTACATATTTGCAACAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAGGCATTTGGTGCTGAT
 AGGGAATGTAGAGAAAGGCTTACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGATGATGACCTGAA
 GCAAAGAGGGGAGAAGAGTGGAAATGAGATCTTATCCCTATATGATGCTGAGAACCAGGCAAGAGCACTTCAG
 AAAACCTGTGCCTCTAGCCCAAGAACCTGAGCGTCACTGCTTCAACCAGTGGGACCAAGGTGACCCCAAGG
 AGCCATGATAACCCATCAAATAATTTGTTCAAATGCTGTGCTCTTCTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCTGATGATGTGGCCATATCTACCTCCCTCTGGCTCATATGTTTGAGAGGATGTACAGGCTGTTGTGTGA
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATTTGTTCCCGCGGTGCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCCT
 GAAGAAGTTCTTGTGTTGAAGCTGGCTGTTTCCAGTAAATCAAAGAGCTTCAAAGGGGTATCATCAGGCATGATAG
 TTTCTGGGCAAGCTCATCTTTGCAAGATCCAGGACAGCCTGGGCGGAAGGGTTCTGTGAATTTGCTCACTGGAGC
 TGCCCCCATGTCCACTTTCAGTCATGACATTTCTCCGGGCAAGTGGGATGTGAGGTGATGAAGCTTATGGTCA
 AACAGAATGCACAGGTGGCTGTACATTTACATTTACCTGGGGACTGGACATCAGGTCAAGTTGGGTTGCCCTGGC
 TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTACAGTGAATGAATGAAGGAGAGGTCTGCAT
 CAAGGTTCAAAACGTGTTCAAAGGATACCTGAAGGACCCCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG
 GCTTCACACAGGAGACATTTGGCTGGCTGGCTCCCGAATGGAACCTTGAAGATCATCGACCGTAAAAAGAACTTTT
 CAAGCTGGCCCCAAGGAGAATCAATGCAACCAAGAGAAGATAGAAAATATCTACAACAGGAGTCAACAGTGTTCACA
 AATTTTGTGACACGGGAGAGCTACGGTCACTCCTTAGTAGGAGTGGTGGTTCTGACACAGATGTACTTCCCTC
 ATTTGCAAGCAAGCTTGGGGTGAGGGCTCCTTTGAGGAACCTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT
 AGAAGACTTGCAGAAAATTTGGGAAAGAAAGTGGGCTTAAACCTTTTGAACAGGTCAAAGCCATTTTCTCATCC
 AGAGCCATTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAGCAAAAGCGAGGAGAGCTTCCAAAATACTT
 TCGGACCCAAATTGACAGCCTGTATGAGCATATCCAGGATAGGATAGGTACTTAAGTACCTGCCGGCCCACTG
 TGCACTGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATTTGTTTTGCCCTTCTCCCTATTTTTTTTTAAAC
 TGTAAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACATATAATGTGTAAACTTAGTTCCCAAATAAATCA
 ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAAGGCTTCAGGGCTACTTTTATCAACATCCCTGTCTTCAA
 GATCCCAGTTTATGTTCTGTGCTCTCTCATGATTTCACACCTTAATCATATTAGTAACCAAGTTCAGGGT
 CAAGGGGACCCCTGTGCTGCTTCTTCTTTGTTTGTGATAAACATAACTTGCCAACAGTCTCTATGCTTATTTACA
 TCTTCTACTGTTCAAACCTAAGAGATTTTAAATCTGTAAAACTGCTTACAAATCATGTTTCTAGTCACTCCAC
 AAACCACTAAAATTTAGTTTGTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT
 CTGCGTAAATTAATTTGTGTACTGAAGGAAAAGTTTGATCATACCAAACTTCTCTAACTCTCTAGTTAGATA
 TCTGACTTGGGAGTATAAAAATTTGGGTCTATGACATACTGTCCAAAGGAATGCTGTCTTAAAGCATTTATTTA
 CAGTAGGAACCTGGGAGTAAATCTGTCTCCCTAGAGTTTGTCTGAGCTGGAAGTGTGTGGGGAGAGAGTTGACA
 GGTGGGCCAGTGAACTTTTCCAGTAAATGAAGCAAGCATGAATAAAAACCTTCTGAACTGGGAACAAGATCT
 ACAGGACGCAAGATGCCACACAACAGGCTTATTTCTGTGAAGGAACCAACTGATCTTCCCCACCCCTTGGATT
 AGAGTTCTGTCTACCTTACCACAGATAACATGTGTTTCTACTTGTAATGTAAAGTCTTTAAAAATAAAC
 TATTACAGATAAAAAA

FIGURE 52

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLLLFTKMLFIFN
FLFSPLPTPALICILITFGAAIFLWLITRPQVPLPLDLNNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTGTGDPKGAMITHQNIVSNAAAFKLCVEHAYEPTDDVAISYLPLAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAPVRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGGRRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNIFYTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALSDGWLHTGDIGRWLPNGTLKIIDRKNIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSLVGVVVPD TDVLP SFAAKLG VKGSFEELCQNQV VREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAARGELSKYFRTQIDSLYEHIQD

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGCCGCGGCAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG
 CCCGGGGCCCTAAGCCATTCTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT
 CCGGT**ATG**GACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG
 AGCTGGTACCTTACCTGGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
 GACAGGGGCCGTGCTTTTCTGCTGGTGAAGTGTCTATTGTCAATATCAAGTTGATCCTGGACA
 CTCGGCGAGCCATCAGTAGAAGCCAAATGAAGACCCAGAGCCAGGACGAAGACTATGATGAGGCC
 CTAGCCCGCCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGGGCTCCTGGACGTAGA
 GGTGTATTCAAGTCGACGAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG
 AGGCCCGGGAGCAGGGCCCGGGGCATCCATGTCTATTGTCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAAACGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTT
 CAACATGGTAGCGCCCGGCCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGG
 TGGAGGGACACATGGGCCTTCGTGGGACGAAAAGGAGTCTCTGCTTCGGGGAGAAACATT
 TAAGTCACCTGCCCTCTCTTCTGGGGGACCCAGTCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCTGCCGCCGGCGC
 TTCTGCAGCAAAAGTTGAGGGCTATGGAAGTGATGCAGCTGAGAGAACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCAGACAACAAGGTCCTCAATGTGCCTGTGGCTGTCTATGCGAG
 GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCCAGGGGGTGTCT
 CCTCAGATGATAACAGTTTTTCATTGACGGCTACTATGAGGAACCCAGGATGTGGTGGCACT
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTCAGTTTCCTGAGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA
 CGGCTGAGGACCCAGCATACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC
 AGGAGGTCTTGTACAAGGAGGAGGCTTGAGCCCAAGTGGCCCTACACCGGAAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACG
 TTTCCCGATCCTACCACTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTTCACGAGGCC
 TACTTCAAGAAGCACAAGTTCAACACGGTTCAGGTGTCCAGCTCAGGAATGTGGACAGTCT
 GAAGAAGAAGCTTATGAAGTGGAAGTTCACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACG
 ACAGCAAGAACCCTTGTGAAGACTCTTTCCCTGCCAGACAGAGGGCCACACCTACGTGGCC
 TTTATTGCAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAGTGCCTCCA
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCCCTGTGGAGATTGTTTCGGAAGAAGA
 ACCACTTCTGGTGGTGGGGCTCCCGCTTCCCCCTACTCAGTGAAGAAGCCACCCCTCAGTC
 ACCCAATTTTCCCTGGAGCCACCCCAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC
ATGAGACCTCCTCCAGGACCCCTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT
 TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTTGTTTTTAACA
 TGAGACTTAATTACTAATCCAAGGGGAGGGTTCCCTGCTCCAACACCCCGTTCTCTGAGTT
 AAAAGTCTATTTATTACTTCTTGTGGAGAAGGGCAGGAGATACCTGGGAATCATTACG
 ATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCCTCACTTTCAGGGCTGGCTCAGAATCTA
 ACCTATTATTGACTGTCTCTGAGGGCCTTGAAACAGGCCGAACCTGGAGGGCTGGATTTCT
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC
 CAACCCATGGACAGGGCCAGCTGGGGCCCATGCTGACACAGCTCACTCAGAGACCCCTTA
 GACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGATTCCAAGCTGGATAGGTT
 GGTCAATTGATTA AAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 54

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
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RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEYSSRSKVYVAVDGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRD'TWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRNRRRRCFSKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNLYRMLRSLLSAQGVSPQMITVFIDGYEEPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFVAVLEEDLDIAVDFFSFLSQSIHLEEDDSLVCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRSLYKEELEPKWPTPEKLWDWDMWMMRPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKEAYEVEVHRLLSAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDDFTTWTQLAKCLHIWDLVVRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

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Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCATAAGAACTGGAAAGCCACTCTCTTTGGAACCCACAC
 CTGTTTAAAGAACCCTAAGCACCATTAAAGCCACTGGAATTTGTTGTCTAGTGGTTGTGGGTGAATA
 AAGGAGGGCAGAGATGGATGATTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGG
 GTGCTGGCCTTCTCTGTGGAAGTGTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA
 GATATTTCTGGGAAAAACACCAAGCAAGTGAACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCCATGAACATGAGCAGCCACGACACACACAGCTGCATGGCTATATTGGTG
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGGTAACTCCCATGTGCATTCT
 ACTGACGATCCAGAGCAGCAAGGCTTAGCAATTCCAAAATCACCACCACGCTGGGTCTGGTTGTCCA
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTGGACTGGTTTCCTTCTTGATGCATGCT
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAAGCCCTTTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTTCTCTGCCGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGCGGGA
 ATAGGACACAGCCACAAGCCCGATGCCACGGGAGGAGAGGCCCTCAGCCGCTTGAAGTGGCAGCCCT
 GGTTCCTGGGTTGCCCTCATCCCTCTCATCTGTCTAGTAGGACACCAAGCATTAATGTTCAAGGTCCAGC
 CTGGTCCAGGGCCGTTTTGCCATCCAGTCAGTGAAGAACGCCGACGTGACAGCTACTCACTTCTCTGCTC
 TCTTGTCTCACTTTCGGCATCTCTACATGTATTCTTAGAGTCCAGAGGGGAGGTGAGGTAAAAACCTG
 AGTAATGAAAAGCTTTTAGATAGTGAACACATTTACGTTCGACATAGCATAGACATCCCATTTGTGT
 TATCTTTTAAAGGCCCTTGACATTTTTCGTTTTTAATATTTCTCTTAACCCTATTCTCAGGGAAGATG
 GAATTTAGTTTTTAAAGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAAATACAGT
 GTTCTGTAATTAAGCTATGCTCTTTTCTTCTAGTTTAGAGGCTGCTGACTTTTATCCATTGATTTTT
 AACATGGTTCCACCATTGTAAGACTGGTGTCTTAGCATCTATGCCACATGCGTTGATGGAAGGTGATA
 GCACCCACTCACTTAGATGCTAAAGGTGATTTAGTTAATCTGGCATAGGCTCAGGAAAATGATAGC
 AAGACACATTGAAAGCTCTCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT
 TAAACAGCTCCTTTGGCACGTGCCTCTCTGAATCCAGCCTGCCATTCCATCAATGGAGCAGGAGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCCCTTGTCAGTTCTCCTTTGCGAAT
 ACCTGCTCCACATCTCTAGAGAGGAGCCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCTTCAAGAA
 CAGTCAGATCACAAAGTGTCTTTGAAAATTAAAGGATATTAAATTTTAAAGTATTTTGGATGGTTAT
 TGATATCTTTGTAGTAGCTTTTTTAAAGACTACCAAATGTATGGTTGCTCTTTTTTTTTTGTTTTT
 TTTTTTTTAATATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACATAAATCACTAGGTCAGTTTT
 GGCACAGCTGTGCTTCTCACATAACCCTGTAGCAAGATGGATCAATAAGTAGAAGTGTGTTGCGCTA
 TTGATTTAAAGCTTATTGGAATCATGTCTCTGTCTCTTCGTCTTTTCTGCTTTTCTTCTTAACCTTT
 TCCCTCTAGCCTCTCTCGCAACAATTTGCTGCTTACTGCTGGTGTAAATATTTTGTGGGATGAATT
 CTTATCAGGACAACCACTTCTCGAAGTCTAATAATGAAGATAATAATATCTTTATTTCTTTATCCCTT
 CAAAGAAATACCTTTGTGTCAAATGCCGCTTTGTTAGGCCCTTAAATACCACCTCCTCATGTGTAA
 ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAGTGTTTAAACAGACTAGGATA
 ATTTTCTTTTTCATATTGCCAAAATTTTGTAAACCTGTCTTGTCAAATAGTGTATAATATTGTAT
 TATTAATTTTATTTTACTTTCTATACCAATTTCAAACACATTTACACTAAGGGGGAACCAAGACTAGT
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTTCTATGACGCATAAGCTAGCATGCCTATG
 ATTTATTTTCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAATAAAGCTTGTGAGCCCTCTGCT
 GGCCACAGTGAGGAAAGTAGCAAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATTGCAATACA
 ATTTTCTACCAAGAGAAGGTATAGTATGGAAGTCCAAATGACTTCCTTGATTGGATGTTAAACAGCT
 GAGTGGTGAGACTTGAGGTTTTCATCTAGTCTTCAAACACTATGAGTTGCCTAGATTCTCTCTGGA
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

FIGURE 56

MDDFISISLSSLAMLVGCVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ
IGNSHVHSTDDPEAARSSNSKITTTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGAGGGCGGCTGCAGAGAGGCGCGCTGGAGCTGAAGA
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACCTTCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA
 TAACATCACACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACAGTTAAAGACCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTCAACAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGAAGGGAAACGTGCTTGTTAACAGCAA
 GTCCAGACACCAGCCCCAGTTCCGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAG
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
 CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTGAGTGAAGAGGCTTCGGGGGAGCCGG
 TGGAGGGCCCTGAGCGAGACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT
 GCCGGGGAAGGGAGAAAACAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
 TGAAGCAGAACTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAAATAGATG
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG
 AATCATACACTCTGAAATTGAACGGAATCACATATTTACAACAGGGCCGAAGAGATGACTA
 TAAAATGTTTCATGAGGGACTGAATACTGAAAAGTGTGAAATGTACTAAATAAATGTACATCTGA

FIGURE 58

MMGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQLQALSEPQFRLQAAGLPHTVEVPQGKGNVLGNSKSQTPAPSSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29



FIGURE 59

GGATG CAGAAAGCCTCAGTGTGCTCTTCTGGCCTGGGTCTGCTTCTCTTACGCTGGCATTGCCCTCTTCA
 CCAGTGGCTTCTGCTCATCCCGTTTGGAGCTCACCAACCTAGACAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
 TGCATCTGGGAGCCCAAGGAAACCTGGGSCCTGCTGGATGGCTTCCGATTTTCCGGGGTTGTGTGGTGTGA
 TAGATGCTCTGCGATTGACTTGC GCCCAGCCCCAGCATTACACGTCCTAGAGAGCCTCTGTCTCCCTACCCCT
 TCCTGGGCAAACTAAGCTCTTGCAGAGGATCCTGGAGATTGACGCCACCATGCCCGCTCTACCGATCTCAGG
 TTGACCTCTCTACCAACCATGCACGCGCTCAAGGCCCTCACCACTGGCTCACTGCGTACTCTTTATGATGCTG
 GTAGTAACCTCCCGAGCCAGCCATAGTGAAGACAATCTCATTAAAGCAGCTCACCAGTGCAGGAAGGCGGTGAG
 TCTTCATGGGAGATGATACCTGGAAAGACCTTTCCCTGGTGCTTTCTCCAAAGCTTTCTCTTCCCATCCTTCA
 ATGT CAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCCCCATGGACAGTGGTGAATGGG
 ACGTGCTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCCTGAAATGGCCA
 AGAACTTAGCCAGATGGACAGGTGATCCAGGGA CTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
 CTGGGACCATGGGATGACCACAATGGAGACCATGGAGGGACAGTGAAGTGGAGGTCTCAGCTGCTCTCTTTTC
 TGTATAGCCCACAGCAGTCTTCCCGACCCCAACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGTC
 CCACGCTGGCCCTGCTGTGGCCTGCCATCCCATTTGGGAATATCGGGAGGTGATGCTGAGCTATTCTCAG
 GGGGTGAGGACTCCAGCCCCACTCCTGTCTTTAGCCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
 CCGGATTTCTTATACCTACTCAGCTGTACTCAGGACCTTCAGGCTAAGGAGCTTTCATCAGCTGCAGAACCTCT
 TCTCAAAGGCTCTGCTGACTACAGTGGCTTCTCCAGAGCCCCAAGGGGCTGAGGCGACACTGCGCATGTGA
 TTGCTGAGCTGCAGCAGTCTCTCGGGGAGCTCGGCCATGTGCATCAGTCTTGGGCTCGTTTCTCTGTGGTC
 GCATGCGGGGGGTACTGCTCTTTGGCTGCTTCTGCTTTATCTGCTGCTGGCATCTGAGCTGGGCAATATCCC
 CAGGCTTTCCATCTTGCCTCTACTCTGACACCTGTGGCCTGGGCGCTGGTGGGGCATAGCGATGCTGGAC
 TCCTGGGAATCTTAGCTGAGCTAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGAGCTCATTCTCCCTT
 TTCTGTGGAAGCCTGGGCTGGCTGGGGTCCAAGAGGCCCTTGGCAACCTGTTCATCCATCCCTGGGCCGCTCC
 GTTTACTCTGCTGTTTGGCTTGGCTGTGTTCTTCTGATAGTTTTGTTGATGCTGAGGCGAGGGCCACCCCT
 TCCTTTTGGGCTCATCTATCTGCTCCTGGTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC
 TCACAGCTGCGCCTTGGCACTTGCACCAACAACCCCCACGGACAATGGTGCATATGCCCCAGGCTTG
 GAATTTGGGTTGCTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTGCCACT
 CCTCTCCCTGGCTGAGTCTCTGGCATCCAATGGTGGGTGTCGAGCCAGAATTTATGGTATGGAGCTTGTGTG
 CGGCGCTGGTGGCCCTGTTAGTGCCTGCGCTGCGCTTGTGGCTTCGCGCTATGGTAATCCAAGAGCCCCGAGCCAC
 CCATGCTCTTTGTGCGCTGGGACTGCCCTAATGGCATTGGGACTGCTGCCACTGGGCATTTGGGCTCGGGG
 CAGATGAGGCTCCCCCGTCTCCGGCTCTGGTCTCTGGGGCATCCATGGTGTGCTGCCGCTGTAGCAGGGC
 TGGCTGCTTCAGGCTCGCGCTGCTCTGTGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCCAA
 GGACAGGACTGTCTCACTCCCTTCTCAGGCCCCCCACTTCTCAAGCTGACTTGGATTATGGTGTCCCTCAA
 TCTACGACACATGCAGGAGGAGTCCGGGGCCGGTTAGAGAGGACCAAACTCAGGGTCCCTGACTGTGGCTG
 CTTATCAGTTGGGAGTCTTACTCAGCTGCTATGGTCACAGCCCTCACCGCTGTGGCCTTCCACTTCTGCTGT
 TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGCTTTCTGCAGAGCTTCTCTTCTCTACATCTGCTTGTCT
 CTGGGATACCCCTCACCACCCCTGGTCTTTTACTGTGCCATGGCAGGCAGTCTCGGCTTGGGCCCTCATGGCCA
 CACAGCCTTCTACTCTCACAGGCCACACGCTGTCTTCCAGCCATCCATTGGGCATGCAGCTCTGTTGGGATTCC
 CAGAGGCTCATGGCTCTGTACTTGTGCTGCTTGGTGTGGGAGCAACACTTGGCTCCCACTCCTCTCT
 TTGCAAGTGTGCCCACCTGCTCTGCTCTGGCCCTTCTGTGTGAGAGTCAAGGCTCGCGAAGACAGACAGC
 CCCCAGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCTGATGGAGATCGGCTCCGGC
 ATGCGCTCAGCACTCTTATGCGCACTGCTCAGCTGGGCTCAAGTACCTCTTATCTGTTGATTCAGATT
 TGGCCTGTGCTTGGCAGCCTCCATCTTCCGAGGACATCATGGTCTGGAAGTGTGTTGCCCTTAAGTTCTAT
 TTGAGCTGTGGCCTTCACTTGTGAGCGTGGGACTTCTCCTGGGCATAGCTTCTGATGAGTGTGATGATG
 CTGTGAGCTCCTGGTT CAGGCAGCTATTCTGGCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCT
 ACAGAGAGTGTGAGAAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGCAGGCTCAGCCATAC
 TCTTACTATCATGCAGCGAGGGCCGCTGACATCTAGGACTTCATTATTCTATAATT CAGGACCACAGTGGATAC
 TGATCTCTAACTCTGATTGGATCTGAGGACAAGGGGGCGGTCTCCGAAGTGAATAAAATAGGCGG
 GCGTGTGACTTGCACCTATATATCCAGCAGCTTTGGGAGGCAAGGTGGGAGGATGCTTGTGCCAGGAGTTCA
 AGACCAGCCTGTGGAACATAACAAGACCCGCTCTACTATTTAAAAAAAGTGAATAAAATGATAATAT

FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWCVCLFYAGIALFTSGFLLTRLELTNHSSCQEPFPGPSLPWGSQKPGACW
 MASRFSRVVLVIDALRFDAFQPHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
 VDPPTTMMQRLKALTTGSLPTTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF
 PGAFSKAFFFPFSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGPHPPEM
 AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAALFLYSPTAVFPST
 PEEEEVIPQVSLVPTLALLLGLPIPFGNIGEVMAELFSGGEDSQPHSSALAQASALHINAQ
 QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
 ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAIISPGFFCPLLLTPVAWGLVGAIA
 YAGLLGTIELKLDLVLGGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGVLLLLLRLA
 VFFSDSFVVAEARATPFLGSGFILLLVQLHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY
 ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPPLASMVGGRAKNLWYGACVAALVALLA
 AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP
 RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
 EFRGRLERTKSQGPLTVAAYQLGSVYSAMVTALTLLAFPLLLHAERISLVFLLLFLQSFL
 LLHLLAAGIPVTTPGPFVWPQAVSAWALMATQTFYSTGHQPVFPAIHWHAAAFVGFPEGHGS
 CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLCESQGLRKRQQPPGNEADARVRPEEEEEEP
 LMEMRLRDAPQHFFYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWKVFAPKFIFEAVG
 FIVSSVGLLLGLIALVMRVDGAVSSWFRQLFLAQQR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
 1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAG**AATGT**
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTGTG
 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCGTGTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGTCACTGGCTGGAGCCGAACACTCTTTACTGCGT
 ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG
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 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGAAATGAATTTGACAAAA
 GATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGAT
 TCTAAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTAG
 GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAAACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCCGGATAAAAACAGTCATTGAATATGA
 ATATGATGTGAGAACCACAGTACATTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGACGGCAGCGTTGGCAGTCTTGGCCCCG
 CAAACGTTACAGTACTCATACCCCCTCAGCTCCAAGACTTAGACCCCCTGCGCAGGAGCA
 CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCTGGTCGACTGGGATCCCC
 AAACGTCAGGCTGTGTATTCCTTCGCTGTCAGCTTCGACCAGGATTCAGAGGGCTGCGAG
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT
 TATATGTGCAGATGGA**AACTGAT**GCCAACACTTCCTTTTGCTTTTGTTCCTGTGCAAC
 AAGTGAGTCACCCCTTGATCCCAGCCATAAGTACCTGGGATGAAAGAAGTTTTTCCAGT
 TTGTCACTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTATTG
 GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGTGGCCGGT
 TGTTCTATGCAGAGAAAGCAGTCAATAAATGTTGCCAGACTGGGTGCAGAATTTATTACAG
 TGGGTGT

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNED
KRFFVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEDVRTTDICAGPEEQELSL
QEEVSTQGTLLSEQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGTGGGCGGCCACGTCTTGAGTACTGCGGAGCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCTGGACTGATGGAGGCCAAGGTCCGAGTGTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGGCACCACAAGACCCCGAC
GTGTACACGAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC
CCAGCCCGGCCCTGCCTGGGACCACCAGGCCCCAGGAGAAGCCGCCT**TGA**GCCACAACCT
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTCAAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAATGTAACTGACAAAAAAAAAAAAAAAAAAGAA

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRLPGRRARPPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLTMLCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA
 CGCCTGTCCCGGCCCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTGCGCGCTGGGCACGGTAG
 CAGGCGCGCCGTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC
 ATCCTTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
 GGAATGGCCAGGAGAGGAGGCAACATCATCTTGGCCTGCCGAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCGGGGAGACCCCAATCACCATGTCAACGCCCCGGCACCTGGAC
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGAAAGATCATTTGAAGAGGAGGAGCGAGT
 GGACATTCTAATCAACAACGCGGCTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
 GCACATAGACTTTGACGACTTGAACCTGGCAGACGAGGAAGTATAACACCAAAGCCGCTACT
 GCCAGAGCAAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCCGACCCCGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG
 CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
 GCCCCGAGCTGGCCGCCAGCCAGCACATACTGGCCGTGGCGGAGGAACTGGCGGATGTT
 TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGGAGGCTGAGGATGAGGA
 GGTGGCCCGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA
 GGGAGCAGCCCCCTCCCA**GA**T**AA**CCCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
 ACCGAGGACAGCTGTCCGCATGCCCGCAGCTTCTTGGCACTACCTGAGCCGGGAGACCCAG
 GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGTGCTGGCCGAGTGGAAGTGGC
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
 AGGGGCCATCTGATGCTTCCCTTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
 TGTGCACTTGCAGGCCACGTGAGGAGGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCTGTGGGACCT
 TGTGCATGCATGGTCTCTCTGAGCCTTGGTTTCTTACGAGTGAGATGCTCAGAATAACTG
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
 GGTGTTTGCTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGCAGGTGCAGGTGTCATCCC
 GAGTTAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
 TTGCCTGGGACTCCACCTTCTATCAATTCTCATGGTAGTCAAACCTGCAGACTCTCAAC
 TTGCTCATTT

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNNARHLDLASLKSIREFAAKIIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLLGHFLLTNLLLDKLGASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGSVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPFIWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQLPR

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTTCGCGAGCGCTGGC**ATG**TGGTCTGGGGCGGGCTGGCGGCGCTGCTGGCGGTGCTG
GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACAGTTCTCGGCGCTGAC
CAGCGTGGCGCGCGCCCTGGCGCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACTCTGC
GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCA
GAGGATTCAACAACCCCTGTGGCTAACCTCTGCTTGCAATTACTCTCATCAAACGCCCTGCA
GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCCTGGCCCGAGGTGTCTT
TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTCTCTCA
CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGATTATTACCATGCC
ATTCCATGGCTGGAGGAGCTGTGAGTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA
GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAA
ATGTTTCGTGTGCCCTCAGCCTCTCTCGGAGTTCCTCTCTACAGCCAGATAATAAGAGG
ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC
TGAGGCTGTCTCCAGAGGCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
TATGTACAGACCTTGGGTTCCAGGCCACTCTCTACCAGATCCCAGCCTCTACTGTTCTCTAT
GAGACCAATTCCAACGCCCTACCTGCTGCTCCAGCCATCCGGAAGGAGGTCTACCACTGGA
GCCCTACATTGCTCTCTACCATGACTTCGTGAGTCACTCAGAGGCTCAGAAAATTAGAGAAC
TTGCAGAACCATGGCTACAGAGGTGAGTGGTGGCATCAGGGGAGAGGAGTTACAAGTGGAG
TACCGCATCAGCAAAAGTGCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCTCAA
CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC
AGCCCCCTCTACAGAAATGAAGTCAGGAAACCGAGTTGCAACATTATGATCTATCTGAGCTC
GGTGGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
GCTGGCTGTCTGTCTGTGGTGGGAGATAAGTGGGTGGCCAAACAAGTGGATACATGAGTATGG
ACAGGAATTCGCGAGCCCTGCAGCTCCAGCCTGAAGACT**GGA**ACTGTTGGCAGAGAGAAGC
TGGTGGAGTCTGTGGCTTTCAGAGAAAGCCAGGAGCCAAAGCTGGGGTAGGAGAGGAGAA
AGCAGAGCAGCCTCTGGAAGAAGGCCTTGTGAGCTTTGTCTGTGCCTCGCAAAATCAGAGGC
AAGGGAGAGGTGTTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
GTCAGAGTAGGATGCACAGTACAAGGAGGGGGAGTGGAGGCCCTGAGAGGGAAGTTTCTGG
AGTTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTGATCAGTGGGTC
TTTTGGCACTTTGAACCTTGACCACAGGAGCCAAAGAAGTGGCAATGAGGACACCTGCAGGAG
GGGCTAGCCTGACTCCAGAACTTTAAGACTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG
CAGGGAGTGTCCCCCTCCAGAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT
TTTAAGTTGAAAACAACTTTCTTTCTTTTGTATGATGTTTTTTTAAACACAGTCATTAAAA
ATGTTTATAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTFVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGWKTEDEASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNI PHLQTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEVAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCTGCTCCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
 ACGAGCGCTGGCTGAGGGACCGAGCCGAGAGCCCCGAGAGCCCCGTAACCCGCGCGGGGAG
 CGCCCAGGATGCCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGCTCAAGTTTTTCACTTATCATCTATTCCACCGTGTCTGCGTGATTGGGGCCCTGGTCCT
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCCTCC
 TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
 ACTTCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
 AACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA
 CCTGTGTCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAACTATCGAC
 AAGGAGCGTTTCAGTGTGCAGGATGTCTATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
 CTGGTTCATGGACAACCTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
 TCTGTCACTGATGGGCTCCTGGGGCCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
 ATGCTGCTTGTGCTACCCCAATTAGGGGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGTCCCACGGCCTCTGCCTC
 CCCAGGGAGCAGAGCCTGGGCCCTCCCCTAAGAGGCTTTCCCGAGGCAGCTCTGGAATCTGT
 GCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGTACAGGGGAGGGA
 GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCCTGGCGGTGGTATTCAA
 GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC
 CTCTTCTCAGCCTCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGGAGCCTA
 GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC
 TAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCAACAGTTTGTAA
 TCAACAATAAAAAACATGTTTTGTTTTGTTTTTAAAAA

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3

MPRGDSEQVRYCARFSYLWKFSLIIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AIIILLGVVMFMVSFIGVLASLRDNLVLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRG IENYYDDLD FKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPG PLACGVPYTC C
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIMEHSVTDGLLGP GAKPSVEAAGTGCCLCYPN

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAGATGGCCGCGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGTCTGGCAGCCACC
 TTGATCCAAGCCACCCTCAGTCCCCTGCACTTCTCATCCTCGGCCCAAAAGTCATCAAAGA
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGTGGGCAGCCTGGTGAACACC
 GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCTCAGTGACTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAAGTGTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC
 AGGTCTGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
 ATCGAGGCTTCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTC
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTTC
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGAAAGGTGACCAAGTGGTTCAATAAC
 TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTACGCCTCATCGTGAGTCA
 GGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTTCATGGTCTGTGG
 ACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA
 GTGAAGCCCTCCGCCCTTTGTTTACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC
 ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG
 AAGGCCTTGGGATTGAGGCAGCTGAGTCTCTACTGACCAAGGATGCCCTTGTGCTTACTCC
 AGCCTCCTTGTGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
 GGAAGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
 CAATAAACACTTGCTGTGAAAAA

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLIILGPKVIKEKLTQELKDHNATSILQQLPILLSAM
REKPPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPLNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTP EFFIDQGHAQVQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLT KDALVLTPASLWKPPSPVSQ

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAAC**AT**GGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCCGTCGCGCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAACATGCATAGACAGTGTGTCGTTTGCAAGCAAGCTGATGAAGAATTCAGATCCTGGC
 AAACCTCCTGGCGATACTCCAGTGCATTCAACACAGGATATTTTTGGCCATGGTGGATTTTG
 ATGAAGGCTCTGATGTATTTTCAGATGCTAAACATGAATTCAGCTCCAACCTTCATCAACTTT
 CCTGCAAAGGGAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTGGAAGAAGTAATATGGAATTTCTCTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCACCGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA
 GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGTCTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTGTATTATTTCTTCAGTTGGATGCTCTCTATTTTAGATCTAAATATCATGGCTAC
 CCATACAGCTTCTGATGAGT**TAA**AAAGGTCCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAAATCGTGTGTGTTTGAAAAGAAGATGCAACTTGTATATTTTGTATTAC
 CTCTTTTTTTCAAGTGATTAAATAGTTAATCATTTAACCAGAAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT
 CCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGTA
 TACTACTTTTGTGTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT
 TTTATATTGCCCTTATCCAAGATGGGAAAGTAAGTCTGACCAGGTGTTCCACATATGCC
 TGCTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCTTTGTGTGGATGTGTAT
 ACTTTACGCATCTTTCTTTTGTAGTAGAGAAATATGTGTGTCATGTGGTCTTCTGAAAATG
 GAACACCATTCTTCAGAGCACAGCTCTAGCCCTCAGCAAGCAGTTGTTTCTCCTCCTCCTT
 GCATATTTCTTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTGTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA
 GATTTAGATTCAATCCATCTCCTTAGTTTTCTTTAAGGTGACCCATCTGTGATAAAAATA
 TAGCTTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAAATGTTTCTACAAATTAGAGT
 TTGTCACCTTATTCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGCGCAGTGACTTACGCTGTAATCTCAGCACTTTGGGAGGCCAAGCAGGCAGATCAC
 GAGGTCAGGAGTTTCGAGACCATCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVMVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWNTNKRFPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPKAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAIVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSDFGRITFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEFFVIYLG LNLPHYPYSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYSSYTKNCTGRFTKKEIKNIRAFYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPILLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL
PQNLSGYSLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**CATG**
 GCCTCTCTTGCCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
 GGTGGCATGCTGCTCCCGAGCTGGAACAAGTCTTATGTCCGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
 TGTGACATCTATAGCACCCCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
 ATCCTTGGAGGCCTCCTGGGATTCATTCTGTGGCTGGAATCTTCATGGGATCCTACGGGA
 CTCTACTCACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTCTGCTCATCC
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT
 ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
 CACCCCAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTCTGTTTTCTCACCTTGCTGCTC
 CCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCCTG
 ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGTCTG
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAGAAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTTATGACTCCACAGTGTCC
 AGACTAATTTGTGATGAAGTGAATAAAACCATCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886

><subunit 1 of 1, 230 aa, 1 stop

><MW: 24549, pI: 8.56, NX(S/T): 1

MASLGLQLVGYYILGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSGKLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAISLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIQVAVNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNYSLSLTGYV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAACGATTTTGTG
TGAAGCTGAAGGTTCAGGGTGTGAATTCCCAGTGCCACTCATCTCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCTTGAGGAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE
 TRQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

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FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGTGCCCTTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTAATGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT
GACCCCTATGGCAACATCAACCCGGCACCACCCAAGGCTGGCTGGGGAACCTTCACCT
TCTGTGAGATTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

amino acids 1-24

Figure 1. The structure of the proposed model.

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCCGCGCCGGCCGCTCCCGCCGCTCCCCGGCACCAGATTCCCTCT
 GCGCGTCCGACGGCGACATGGGCGTCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGA
 TCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCGGTGGCAGCCTTCAAGGTCG
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTCACCCCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCAGCCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG
 GATAGCGGCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCATCGGAGCACAGGGT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAAGTGTGTGGTGT
 ACCCATCTCTCTCCAGGATAGTGAAACATCAGGCTGCAGCCCTGGCTACGGGTGCCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCTGCTCTACAAGCAAAGGCAGGCAGC
 TCCAACCGCGTGCACAGGAGTGGTGGGATGGACAGCAACATTCAAGGGATTGAAAACC
 CCGGCTTTGAAGCCTCACCACTGCCAGGGGATACCCAGGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGCCCCAGCGCAGCCTTCTGAGTCTGGCGGGCATCTGCTTTTCGGAGCCCAGCAC
 CCCCCGTCTCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCTGTCCCTGACT
 CTCCAAACTTTGAGGTCATCTAGCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGCTCTG
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCAGCCCTCAACCCCTC
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGGTGTGAG
 ATTCTCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGGCACCCCTCCCAGGCACCAGACACAGGGCACGGTG
 GAGAGACTTCTCCCCGTGGCCGCTTGGCTCCCCGTTTTGCCCCAGGCTGCTCTTCTGTCT
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCCTGCCCTGCCACTGGCCATCGCC
 ACCTTCCCCAGCTGCCTCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
 ATATTGGGCATGGTGGCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCCACCCACTGGAGATGGTGTCTGAGGAGGTGGTGGGGCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCATCCCTACTCCCACTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACAAATGTCTTGCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAAAACTACATGGGGAAAAA

FIGURE 84

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRRAQELVRMSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
 TTCCC CGGTTCCTCTTTCCACCTTTCTCTTCTCCACCTTAGACCTCCCTTCTTGCCCTCC
 TTTCTGCCCACCGCTGCTTCTTGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCTCCCGA
 CTCCTGCTCCCGACAGCGGCCTGACCTGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCT
 TCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCCGCCC
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
 TGTACC GCCTCCACTGTCCGCCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCCTCTGGACTCCGGGCCCCACCAAGTCTTGCC
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC
 CGCCTGCCCAACAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
 AACCTGCCCCGAACCAGGCTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGCACTCGCTCCATGGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC
 CCCCCTGGCCTCAGCGCCCCCTGAGCTTCATCCCTCGCCACTTCAGACCCAGGGAGCAG
 GCAGCACAACGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
 AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCTGTCCTTCGGCCCCCTTGCCCTG
 CATCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCCGAGT
 ACCCTTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGGACAAA
 GCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCT
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCAGAAAGAGGCACAGCACTCCGACTGCTCGCTGGCCCCAC
 GAAGTCACTGGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTACAGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 86

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRRHPQDPCSSDAGRKRGGT PAPTGLSAPLSFIPRHFPRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHFAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPKVVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPDG
AEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 87

FIGURE 88

MDSL RKMLISVAM LGAGAGVGYALLVIVTPGERRKQEM LKEMPLQDPRSREEAARTQQLLLA
 TLQEAATTQENV AWRKNW MVGGEGGASGRSP

Signal peptide:

amino acids 1-18

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FIGURE 89

[illegible]

FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLLILFLLSWGPLQGQHHLVEYMERRLAALEERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETONPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVRFPPWVGTLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCIAKLDLPQTLDTEQ
QWDTPCPRENAEAAAFVICGTLVYVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCTCTCTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCTGTCT
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGETTCTTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGTGAAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTGAGCACTGGGCTCAGTTCTCTCATTTCATCCAGGATATGTT
 GATAGAGACATCCAGCTACTCTGTGAGTCTCCTCGGGCTGGTTCCCCCGGCCACAGCAAGTG
 GAAAGTCCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTGTTGATGTGGAGATCTCTGTGACCGTCCAAGAGAACGCCGGGAGCATATCTGTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACTTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACCTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAAAACATTACTGGGAGGTGGACGGAGGACACAATAAAGGTG
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGGTACTGGGTCTCTCAGACTGAATGGAGAACATTGTATTTACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCC
 ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGCCAAAGGGCCTCTGC
 AATCCAGAGACAAGCAACAGTGAGTCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGG
 GTGAAATGTAGAGTGAATCACATCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCA
 GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTGATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGTGGAAGAACC
 TCAGGAATCCCATCTCAGAGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGTTTGTTCATTATATTACACTTTCAGTA
 AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCLSPKTNAEAMEVRFRRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFFRPTAKWKGPGQDLSTDSRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAEALRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRNLNGEHL YFTLNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSESSSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCATGGTGCGCCCGGTGGCGGTGGCGGCGCGGTTGCGGAGGCTTCTTGGTCGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
CATGGAGGAGCCTGCCGAGCCTGGGCGGCCCTGCCCTGTGTGCTGCGCCGCCGCCGCCGCCG
 CCGTCGCCTCAGCCGCTCGGCGGGGAATGTACCGTGGCGGGCGGCCGCCGCCGCCGCCG
 GACGCGTCGCCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCCTAGGGCGACGGC
 TCCCAGGGCCAGGGCCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTCC
 ACCACCTTTTCAGCGCCGCTCGGCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACCTT
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCCTTTCGACGACCACTGGCCCGG
 CGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGACTCCCCGGACCCCGACCCCG
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCTCCCCACCCACCTGCCACCGAGGCCCCCTC
 TTCGCCTCCTCCAGAGTATGTATGTAATGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAC
 TGCAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCCGTGCAACAGG**TAA**GCAACAGAGGGTGGAAGCTGAAGTTTATT
 TTATTTTAGCAAGGGGAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
 GAGGATGAGGTCATAGATTTACAAAATATTTATATACTTTTATTCTCTTACTTTATATGT
 TATATTTAATGTGAGGATTTAAAAACATCTAATTTACTGATTAGTCTTCAAAAGCACTAG
 AGTCGCAATTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTTATGAAGAA
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT
 ATGTTTATTAATATACCATTGGAGTTTGAGGAAATTTGTTGTTGGTTTATTTTTCTCTCTA
 ATCAAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACTGGGGTACCCTAATTTA
 TTTAACTAGTGGTAACTAGACTGGTTTACTCTATTACCAGTACATTTTGGAGACAAAAG
 TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA
 ATAATGTACTGTTATCTAAGCATTGTCCTTGACTGCAGTGAAGTAATTTCTTTGACCT
 TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACCTGAAGAGACAGTATTAAT
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACTGGGTATAACCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTTGGGCAAGTAATTTCCCTTTCAGTGAAGCTGTTTCTTCTCAAG
 GTTGTGTGAAGATTAAATGAGTTGATATATATAAATGCCTAGCACATGTCACTCAATAAA
 TTCGTGTTTTGTTTTAATTTCAAAGGAATATTATGGACTGAATGAGAGAACATGTTTTAAGA
 ACTTTTAGCTCCTTGACAAGAAGTGCTTTATACCTTTAGCACTAAATATTTTAAATGCTTTA
 TAAATGATATTACTGTTATGGAATATTGTATCATATTGAGTTTATTAATAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCAGCCTGTAACTCCTAGCACTTTGGGAGGCCAAGCGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTCTACTAAA
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT
 GAGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGTTGCAATGAGCTGAGATCGCGCCACT
 GCACCTCCAGCCTGCTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 94

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSPLGGLALLCCAAAAAASASAASAGNVTGGGGAAGQVDASPGPLRGEP SHFFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTP LWATAGPSSTTFQAPLGPSPTTPPAAERTS
TTSQAPTRPAPTTLSTTTGPAPTPPVATTVPAPTT PRTPTPDLPSSSNSSVLPTPPATEAPS
SPPPEYVCNC SVVGS LNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLN YTSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGGATGGGGCGCCCTGCTGCTGGCTGCTTTTCTGGCCTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCTCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTTCATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC
CTGGGCTTCTGTACAGTTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAGAT
CCTTCTGTGAGTGTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT
CACAGCA

FIGURE 96

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FIGURE 97

AACAGACGTTCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTT
 CCGTGACGTTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
 GGCTGGATTATACCTGGCCAGTAGTTCATGGCTACTGGTTCGGGAAGGGGCAATACAGA
 CCAGGATGCTCCAGTGGCCACAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCAG
 GCACCTGGAGTCCGGCTGCCCCAGAACTGACCTGCTCTGTGCCCTGGGCCCTGTGAGCAG
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTTAC
 CCGCCTCAGAAGTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCCTGACCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
 ATTACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCTGTCTTCTGCGTCATCTTCTGTTGTAGTGAGGTCCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCTGGGAGATACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTGAGCCT
 CTCAGGGGCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCTCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGATTGAAAACTGCAGAGACTCACCTGATTAGGGATCACAGCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPFVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYPKHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTTPMISWIGTSVS
PLDPSTTRSSVLTLIPQPQDHGTSLTCQVTFPGASVTNKTVHLNVSYPPQNLMTVFQGDG
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSLSQSKATSGVTQGVVGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDGTGIEDANAVRGSSASQGPLETEPWAEDSPFDQPPPASARSSVGEGLQYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

[illegible]

FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:**Signal peptide:**

amino acids 1-17

FIGURE 101

GTTCCGAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA
 TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTGAG
 TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAAGACGCGGCTACTCTGTGG
 GCGCAGCTCATGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGTACA
 TAGTTCACCTGGGGCAGCACACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
 CATCATGTCTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCAGCTCC
 AGCCCCCAGTTACGCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA
 GAAGTGTGAGAACGCTACCCCGGCAACATCACAGACCATGTTGTGTGCCAGCGTGCAGG
 AAGGGGGCAAGGACTCCTGCCAGGGTGAATCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTT
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATACCCGAAAGCCTGGTGTCTACAC
 GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCA
 CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGGTTCCTGTTCACTCTGTTAAT
 AAGAAAACCTAAGCCAAGACCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
 CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTTGCCTT
 GAAATATGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCAGCCCCA
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSTITW
AVRPLTLSSRCVTAGTSCGISGWGSTSSPQLRLPHTLRCANITIIIEHQKCENAYPGNITDTM
VCASVQEGGKDSCQGDSSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTTCGCTGGAGCCGATGCCAAAAACCATGCATTTCCTTATTCAGATTCATTGTTT
 TCTTTTATCTGTGGGGCCTTTTACTGCTCAGAGACAAAAGAAAGAGGAGACACCGAAGAA
 GTGAAAATAGAAGTTTTCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT
 ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCCTACTGCAGCCGGA
 CACAAAATGAAGGCCACCCCAATGGTTTGTTCTTGGTGTTGGGCAAGTCATAAAAGGCCTA
 GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
 TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTGG
 AGATTGAACTTTATGCTGTGACCAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
 ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
 AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTTAAGA
 AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
 GAACTATAGCATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
 AAACAAAGTCACTTTCTCCAAGTTGTATTTGCTATTTTTCCCTATGAGAAGATATTTTGA
 TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACTTAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLGWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDFISPKEYNVYQHDEL

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSRL

Signal peptide:

amino acids 1-18

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FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC
 AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCAGACTTTGGAAGTGACCCACC**CATGG**
 GGCTCAGCATCTTTTGTCTGTGTGTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
 CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
 GCGGCAGCAGGTA CTGGGTGCGCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCGCTCCGCGTAACCAGCAGCGTTCAAC
 CCTGCCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
 ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCTCAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCAGAGCAACATGGTGTGTGCAG
 GCGGCGTCCCGGGGCAGGATGCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
 GTCTTCAAGGTCTGGTGTCTGTGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACA**CTGAC**
 CTGTTTCCTCCACCTCCACCCCCACCCCTTAACCTTGGGTACCCCTCTGGCCCTCAGAGCACCC
 AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTGTGTGGCCTGGGAACCTTCTTGGAACCT
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAAATATAAATGAAGGAGGGGCACAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPNPFDDLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSGVPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

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FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCCTCGC
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGGAAGGCGTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC
 GAGATCAACCGGAGTTCCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
 GCTCAGACCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
 TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAA
 CATGATGCTGGGGAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**
 GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTGTGTGTTT
 TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC
 TGAGCCTTGGGTCCCCCTCCCTCTCTTCTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG
 ATATCAAACCAAAAAGTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
 CTCACCTTGAGGAACCAGCACTCTCCATCCTTTTCAAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGCAGGGCCTCTTTCGGGTTTTCCTTGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC
 AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCACTCATTCCACACCTCTTCT
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
 TACCAGAAGGAACCTCCAGTCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
 GGGTTTGGGGGGAAGGTGAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGGTGCTTGCTGTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV
MFEGKANESSEKPVGPPPERDIASLP

FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA
GGAGCGGGGCGCTGCACACCATGGGCCCCGGGTGGGCAGGGGTGCGCGCCGCCGTGCGCGCC
CGCCTGGCGCTGGCCTTGCGCTGGCGAGCGTCTTGAGTGGGCCTCCAGCGCTGCCTGCC
CACCAAGTGTACTGCTCGCTGCCAGCGTGGACTGCCACGGCTGGGCCCTCGCGCGGTTCT
CTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCATCTGGAGAACACAGGT
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCCTTGAACA
AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA
GATTTGAGTGAACCAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCAGTGT
GAAGAACCTGCAACTGGACAACAACCATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGC
TTCAACCACATGCCGAAGATCCGAACCTCGCGCCTCCACTCCAACCACCTCTACTGCGACTG
CCACCTGGCCTGGCTCTCGGATGGCTGCGACAGCGACGAGTGGCCAGTTACACTCT
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG
TGCCAGCCCCCACTCGGAGCCCCATCCTGCAATGCCAACTCCATCTCCTGGCCTTCGCC
CTGAGCTGCAGATAAATCCTCCAGGCGCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA
ACTTGCCGGAGGGCATCGTCAAAATACGCCTAGAACAGAATCCATCAAAGCCATCCCTGCA
GGAGCCTTCACCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGATCAGATATCGGA
TATTGCTCCAGATGCTTCCAGGCGCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA
AGATCACCGAGATTGCCAAGGGACTGTTTGTATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
AATGCCAACAAAGATCACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACT
GCTCCTCCTGTATGACAACAAGTGCAGACCATCAGCAAGGGGCTTCCGCCCTTCCGAGT
CCATCCAGACCTCCACTTAGCCCCAAACCCATTTGTGTGCGACTGCCACTTGAAGTGCTG
CGCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCGCTGCAGCAGCCCGCGCG
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
ATTACCGCAGCAGGTTCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCGGAGAAGGTGCG
TGTGAGGGCACGATTGTGAGTGTCTCAACCAGAAAGCTGCTGCAGTATCCCAAGCCACCTCCC
TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
TCTTCAAGAAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAAACAATAAGATCAAGGAGGTG
CGAGAGGGAGCTTTTCGATGGAGCAGCGAGCGTGCAGGAGTATGCTGACAGGGAACCGT
GGAGACCGTGCACGGGCGGTGTTCCGTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCCGTTGAGACTGCT
TCCCTCATGACAATCGGATCACCACCATCACCCCTGGGCGCTTACCACGCTTGTCTCCCT
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCTAGGTGCCAGAGGCCATTTTTCCTC
AAGGAGATTTCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
TAGCTGCCAGCTGAGCCCCGCGTGCCCGGAGCAGTGACCTGTATGGAGACAGTGGTGGAT
CGAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC
CTGGAAGAAACCACTAACAGCCGTGCCAGAGAGCTGTCCGCGCTCCGACACCTGACGCT
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
ACCTCTCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGCTCCACGCCTTCAAC
GGGCTGCGGTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTTCTGAAGG
CTCCTTCAACGACCTCACATCTCTTTCCCATCTGGCGCTGGGAACCAACCCACTTCCACTGTG
ACTGAGCTTTCGTTGGCTGTGCGAGTGGTGAAGCGGGGTACAAGGACCTGGCATCGCC
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACGCTT
CCAGTGCAAGAGGCGCAGTGGAATCAACATTGTGGCCAATGCAATGCCTGCCTCTCCAGCC
CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCTGCCCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGCCCTC
 TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCAGATGACTGTGAGGACAACTGCTGCGAA
 AACAAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCTGAGCTGAACCTCTGTGAGCATG
 AGGCCAAGTGCATCCCCCTGGACAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCTTCTGTG
 AACACCCCCACCCATGGTCTTACTGCAGACCAGCCATGCGACCAGTACGAGTGCCAGAAC
 GGGGCCAGTGCATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCGG
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAGACTCCTACGTGGAACCTGG
 CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
 GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT
 GCGGCTGGTCTATGACAGCCTGAGTTCCCCCTCAACCACAGTGTACAGTGTGGAGACAGTGA
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCCTGAACCTAGTAGTG
 GACAAAGGAACCTCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCTCTCCGCCTTGCGCCAGGGCACGG
 ACCGGCTCTAGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG
 GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTTGCACCGT
 GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAC
 GCTGGACCGGCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC
 CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGAAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC
 GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCATCATGGAATGTGTTGGGGGCT
 GTGGGCCCCAGTGCTGCCAGCCCACCCGACGCAAGCGCGGAAATACGTCTTCCAGTGCACG
 GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGGCGCTGCCTCGCGTGTTC
CTAAGCCCTGCCCCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
 ATGTGGGACCCCTGTTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAGAAGA
 AGAGAATATTAAGTATATTGTAATAATAACAAAAATAGAAGCTAAAAAAAAAAAAAAAAA
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FIGURE 112

MAPGWAGVGA AVRRLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRLNKNKLQVL
 PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRLVTSFNHMPKIRTLRLHSNHLCDCHLAWLSDWLRQRRTVQGFTLCMAPVHL
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFTQYKKLKRIDISKNQISDIAFDAFQGLKSLTSLVLYGNKITEIAK
 GLFDGLVSLQLLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL
 AQNPFVDCCHLKWLDADYLDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDRLRNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTMLRSNLISCV
 SNDTFAGLSSVRLLSLYDNRIITITPGAFTTLVSLSTINLLSNPFCNCHLAWLGKWLKRKR
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETTVRCSNKGRL
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL
 SYNRLRCIPVHAFNGLRSLRVLTTLHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCSLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFQCKGPVDINIVAKCNACLSPPCKNNGT
 CTQDPVELYRCACPYSYKGKDCTVPIINTCINPCQHGGTCHLSDSHKDGFS CSCPLGFEGQR
 CEINPDDEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLQHEAKCIPL
 DKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGGSGPFCEHPPPMV
 LLQTSPCDQYECQNGAQCI VVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS
 VELVTLNQTLNLVVDKGT PKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIEHVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCERPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKAEGYGGDLCDNKNDSANACSAFKCHHGQCHISD
 QGEPYLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCCCTGAGCTGCCTGTACCGACTAGGTGGAGCAGTGTTCCTCCGCA
 GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCCTTTTCAGTTCTGTCT
 CCGGCAGGCTTTGAGG**ATGA**AGGCTGCGGGCATTTCTGACCCTCATTGGCTGCCTGGTCACAG
 GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG
 GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA
 CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
 ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTGCCTGC
 TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
 GACACAAGGAATGAAGTATTTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
 AGTGGA AAAAAGGCTGTGAGGTTTCCT**TAA**ACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC
 GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTATCTTGTCCCGTTTCCTCCCAATA
 TTCCTTCTCAAACCTTGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT
 TTAAATGTC

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

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FIGURE 115

CAGGCCATTTGCATCCCACTGTCTTGTGTTTCGAGCCAGGCCACACCGTCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAAAACTTGTACATGGCTCCC
 CATTGGTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTT
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGTCACTTCCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCTGATGTCTCTATCCATCTCTAAATGTACCAG
 CTTTGACTCAGTTGTTCTGAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC
 CTCTCCACAGCTGCACGTGTGTCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCCTTGAGT
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTAT**TAA**TCAGATTGTTTTTAAGATCTCCATTAATGTCAATTTTTATGGATTGTAGACC
 CAGTTTTGAAAACAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA
 AACCATGTCTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTACAGAGAGTATTTAATATATTTTCTCGGGATTATTGCTCTTCTGTCTA
 TAAATTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTAAGTGTGTATCATTATCAA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTCCCAGATTCAAT
 CCACCGAAGTGTTCACTGTCATCTGTTAGGGAATTTTTGTTTGCCTGTCTTTGCTCGGATC
 CATAGCGAGAGTGCTCTGTATTTTTTTTAAGATAATTGTATTTTGCACACTGAGATATAA
 TAAAAGGTGTTTATCATAAAAAATAAAAAAAAAA

FIGURE 116

MPLLLKLVHGSPLVFGEKFKLFTLVSAIPVFRRLARRRKKILFYCHFDPDLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCA**ATG**TGGACTTCGCGATCTT
 CGCGCTTACCTTCTTGTGCGGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAGTTTGCATGAGTTCTCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACCTGTTGATGTACTGAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAACACCATGAGGAAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACCTTTGCCCTCCTCCTAAGCTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTCGCCCTCAGCCAGCATATGCTTGGTTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTGGAAGATGATCAGGAAGTCATTGCG
 CTTCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAGAGGCTTTCAGATGGGTCAC
 TTGATAAAAAACATGACTCGGAAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTTGGAAATGGTCCTGTTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAAACTGTTCGAACTGCCA
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT
 CCTAGAGAGACCCCTCGTCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGTATCCAGATCGGTTTGATGATGAATTAGTAATGAAACTTTTTCTCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGATATATGGTGACCACA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTCTGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 AT**TAAA**AATTTTATACATTTAAAATCATTTGTTAAATTGATTGAGGAAAAACAACCATTTAAAA
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLLVSLGTVDVLKQHINPNKTSDFETMLKSLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIRFQKNHGTVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTGTGCGCCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA
 GACCGCCGCCCTTGTCCCCGAGGGCC**ATG**GCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
 CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGACAGCAACAT
 ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTACAGCTGG
 TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
 GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
 GGCCCTGTCCCTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTGTCT
 TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAA
 AAGAAACCTTCT**TGA**TACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
 CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTCCCTCGGAAACTGCTTC
 TGCTGGAGGATATGTGTTGGAATAATTACGCTCTGAGTCTGGGATTATCCGCATTGTATTTA
 GTGCTTTGTAATAAAATATGTTTGTAGTAACATTAAGACTTATATACAGTTTtaggggaca
 ATTAAAAAAAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
 LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT
 EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

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FIGURE 121

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 AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGACGTGGGCTAC
 AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTTCACGGGTGC
 CCACTCAGGTCACCTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
 ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT
 CAGGGAGCCCTGAGGTCCAACCTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
 TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTGAGGCC
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FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNMMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

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FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT
 GACTCGCTGCTGCTTCTGTTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGCCCC
 CGGGTGCCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCC GCCCATGGCCAATTCCACTCT
 CCTAGGGCTGCTGCCCCGCTGGGGAGGCTTGGGGCATCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCAAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCGGACCTC
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCAGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACTACCATAGTGATACCCCTACTACCCATC
 TGGG**TGA**CCCGGGGAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCCTCAGGCAGGGAGGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGTTCCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGAAGTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
 CTCTGTGCAGCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCATT
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC
 ACAGCCCATCCGCGTGTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGAGACCGGGTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCCGGGCCGAGA
 GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT
 GAAACCCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAGCTT
 GCCCCGGGGCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MLTRCCFVFLVQGSlyLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY
YPSG

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACAGAGTGGGTGCAGGGGCCCCA
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAGGGTTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGGAAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCAGACACCGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC
 GGCTGCGGCTGCCCACACGGCTCACCATGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
 GCCGTGCTGCTGGTCTCACGCTGCCGGGGCTGCCGCTCTGGGCACAGAACGACACGGAGCC
 CATCGTGCTGGAGGGCAAGTGCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
 GCTCCTCTTCTCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCTTCTCG
 GCGGTGCGGAGCACCAACCAGAGCCATCCGAGATGAGCAACAAGCGGCATCATTTACTT
 CGATCAGATCCTGGTGAATGTGGTAATTTTTTTCACATTGGAGTCTGTCTTTGTAGCACAA
 GAAAAGGAATTTACAGTTTCAGTTTTTCACGTGATTAAAGTCTACCAGAGCCAACTATCCAG
 GTTAACCTTGATGTTAAATGGAAAACAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGGAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTTCTGGTG
 TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAGCTGTCTGCAAGACTTATTCTGAATTTCAATTTCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACCTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTGTTTGGTTCTTGTA
 AAACTTGGATTTTTTTTTTTCAGTAACGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
 TGGCTTGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA
 GAATGCTTCATAGTTGTATTTTAAATGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
 TTCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCCTCGAGGGAATCTTATACTTTATTGC
 TCAACTTTAAATTAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTTT
 TCCGTAGACATGACCACTTTATTAACCTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTTGATTATTGAAGTATCATCTGTTTTGCTTAACTCTTTAAATTGTA
 TATATTTATCTGTTTAGCTAATATTAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
 CTGTGCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAA

FIGURE 126

MGSGRRALSAPVAVLLVLTLPGLPVWAQNDEPIVLEGGKCLVVCDSPATDSKGSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTTLESVVFVAPRKGISFSF
HVIKQVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

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FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATGTATTTTTTGATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTTTACAACCAGCGCTCCAGATAACCTCAGGGAACCAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTCTGAAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 128

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFIAAGGSCRSCLKCLLCQDKN
FLLYNQRRSR
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCGCCGCCACCAACCGCTGCCACTGCCGCCCTGCCGGGGCC**ATG**TTGCTCTGGGCTTGGCCCTTCT
 TGGTGTCTTGGTGGCCCTCGGTGAGAGGCCATCTGGGGGTCTGGGGGCCAAGAACTCTCGCAGAAAGACGCCG
 AGTTTGAGCGCACTACGTGGAGCAGGTTCAACAGCGAGCTGGTCAACATCTACACCTCAACCACTACTGTGACCC
 GCACAGGACAGAGGGCGCTGGTGTGTCTGTGAACGCTCTGAACAGCAGAAAGGGGGCCGCTGTGCTTGTGGT
 TCCGCCAGAGAGGGCTGTGGTGTCTCTCCAGGTGCCCTTAATCTCGCAGGGGATGTTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGGAAAGCAACCTGTGTGAGCCCCCACCAGAAATGAGTGGGAGATGATTCCTTCTACGTTGGATG
 TGTCCACCTGTCAACAGTCAACACCATACCAAGCTCCGGGTGAGCCGATGGAGCATTTTGTGCTCAGGACTG
 GGGAGCAGTTCACTTCAATACACAGCAGCAGACGCCCACTACTCAAGTATGAGTTCCTGTGAGGCGTGGACT
 CGGTAATTGTCAAGGTGACCTCCAAACAGGCCTTCCCTGCTCAGTCAATCCATTTCAGGATGTGCTGTGCTCTG
 TCTATGACCTGGACAACAGCTAGCCTTTCATCGGCATGTACCAGACGATGACCAAGAGGGCGGCCATCACCGTAC
 AGCGCAAGACTTCCCAGCAACAGCTTTTATGTGTGGTGGTGGTGAAGACCGAAGACCGCTCGCGGGGGCT
 CCTGCCCTTCTACCCCTTCGCAGAGATGAACCGGTGATCAAGGGCACCGCCAGAAACCCTGTCAGTGCTGG
 TGTCTCAAGCAGTCACTGTGAGGCATACGTGAGTGGGATGCTCTTTTGCTGGGTATATTTCTCTCCTTTTACC
 TGCTGACCGTCTCTGGCTGCTGGGGAACCTGGAGGCAGAAAGAAAGACCTGCTGCTGGCCATTGACCGAG
 CCTGCCCAAGAAAGGGTCACTTCAGTCTCTGGCTGATTTCTTTCTGGCAGTTCCCTTATGAGGGTTACAAT
 ATGGCTCCTTTGAGAATGTTCTGGATCTACCGATGCTGTGGTTGACAGCGCTGGCAGTGGGACCTCTTATAG
 GTTACCAGGGCCGCTCCTTTGAACCTGTAGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGATG
 ATCAACACACATTGACCGCATCGATTCCGACAAAGAATGTCACTCGCACCAAGCAATACCTCTATGTGGGTGACC
 TGCACCGGAGGACAGCCGCTGTTCTCGGAAAAAGTACCAGATCTACTTCTGGAACTTGCCCAATTTGCTGTCT
 TCTATGCCCTTCTGTGGTGCAGCTGGTGATCACTACCAGACGGTGGTGAATGTACAGAGGATCAGGACATCT
 GTCATCAACTTCTCTGGGCCACCCACTGGGCAATCTACGGCCCTTCAAAAGATCTCAGCAACTCTGGGGT
 ACATCTGCTGGGGCTGCTTTTCTGCTCATCTCTGCAACGGGAGATCAACCAACACCGGGCCCTGCTGGGCA
 ATGACCTCTGTGGCCCTGGAATGTGGGATCCCCAACACTTTGGGCTTTCTACGCCATGGGCACAGCCCTGATGA
 TGGAGGGGCTGCTCAGTCTTGTCTATCATGTGTGCCCAACTATAACAAATTTCCAGTTTGACACATCGTTCATGT
 ACATGACCGCGGACTGTCATGCTGAAGCTTACACAGAGCGGCACCCGACATCAACGCCAGCGCTCATGATG
 CCTACGCTGCTGCCCATTTGATCATCTTCTCTCTGTGCTGGGCGTGGTCTTTGGCAAGGGAACAGCGGCTTCT
 GGATCGTCTTCTCCATCATCATCATCGCCACCCTGCTCCTCAGCACGCACTTAATACATGGCCCGGTGGA
 AACTGSACTCGGGGATCTTCCGCCCATCTCCACGCTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGC
 TCTACGTGGACCGCATGGTGTCTGGTCATGGGCAACGTCATCACTGGTCTGCTGGCTGCTATGGGCTTATCA
 TCGGCCCAATGATTTCGCTTCCGACTTGTGGCCATTGGCATCTGCAACCTGCTCCTTTACTCTGGCTTCTACA
 TCACTCATGAAGCTCCGGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTTTGCACTCCGTGGTCT
 GGGGCTTCGGCTCTCTTCTCTTCCAGGGACTCAGCACTTGGCAGAAAAACCCCTGCAGAGTCGAGGGAGCA
 ACCGGGACTGCATCCTCTCGACTCTTTGACGACCACGACATCTGGCACTTCTCTCTCCATCGGCATGTTCG
 GGTCTTCTGGTGTGCTGACACTGGATGACGACCTGGATACTGTGCAGCGGGCAAGATCTATGTCTT**TAGC**
 AGGAGCTGGGCCCTTCGCTTCACTCAAGGGGCCCTGAGCTCCTTTGTGTGATGACCGGTCAGTCTGTCTGTCT
 TGGGGATGAGTCCCAGCACCGCTGCCAGCACTGGATGGCAGCAGGACAGCTGAGTCTTAGGCTTAGGCGCT
 GGGACAGCAGTGGGTGGCATGGAACTTGCAGTGCCTCTGCCGAGGAGCAGGCTGCTCCCTGGAAACCCCC
 AGATTGTGGCCAAATTCGCTCTTCTCTCAGTGTGGGGCCTTCCATGGGCCCTTGTCTTGTGGCTCTCAATTT
 GTCCTTTTCAAGAGGAGGATGGAAGGCAACCTCCCACTTTCATGCTCTGCATTTTGCCCGTCTCTCTCCC
 ACAATGCCACGCTGGACCTAAGCGCTCTTTTCTCTCCATCTCCCATCCAGGGCCTAGTCTGGGGCTGA
 ATCTCTGTGCTGTATCAGGGCCCAAGTCTCTTTGGGCTGCTCCGTGGCATCTGCTGCATCTCCAGTCCAGTCCAGC
 AGGATGGATGGGGGTATGAGATTTGGGGGTGGCCAGCTGGTGGCAGACTTTTGTGCTAAGGCCTGCAAGGGG
 CTTGGGGAGTGGGTATTTCTCTTCCCTGACTGAGTGTGCTCAGGGCTGGCTTTTAGCAATGGCCTCAGGCCGT
 TGAGAACCCCTTCTGATTCAAGAGGCTGAATTCAAGAGTCACTCTTCAATCCATCAGCTCCAGACTGATGCC
 AGCACAGGACTGGAGGGAAGCGCTCACCCCTTCCCTTCTTCTTCCAGGCCCTTAGTCTTGGCAACCC
 AGCTGGTGGCTTTCAGTGCAATTGACACTGCCCAAGAAATGTCCAGGGGGCAAGGAGGATGTACAGAGTTGAG
 CCGGTTCTGCTTCCACAGTGTGGGCACCCAGTGCCTACCTTAGAAAGGGGCTCAGGAAGGATGTGCTGTGTT
 CCCTCTACGTGCCAGCTCTAGCTCTGCTCTAGGACCCAGGCTGGCTTCTAGATTTCGCTCAGTCTTTCAGCA
 AGTTGTGTTAGTCAATGCACACATCACTATGAACCTTGGAGTTTACAAAGAAATGGCCAGCTCTGGGCAC
 CCTGGCCACCTGTGCTTGGATCCCTTCTGCTCCCACTGGTCCACCCAGTGGATGAGATGGGGAGCTCAGG
 CGGGCTCTGCTTTGGGGATGGGAATGTGTTTTTCTCCAACTTGGTTTATAGCTCTGCTTGAAGGCTGAGG
 AGATGAGGTGGTCTGGATCTTTTCTCAGAGCGTCTCCATGCTATGGTGCATTTCCGTTTTCTATGAATGAAT
 TGCATTCAATAAACACAGCACTCAAAAAAAAAAAAAA

FIGURE 130

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVNLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTEGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFFPCSVISIQDVLCPVYDLDNNAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSILPFYPFAEDEPVDQGHRQKTL SVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLTLLVAIDRACPESGHPRLVADSFPGSSPYEGYNGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGT RPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVNVNTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCPNYTNFQFDTSEFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNATFAWIVFSIIHIIATLLLLSTQLYMGWRKLDSGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFFFQGLSTWQKTPAESREHNRCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDLDDLDTVQRDKIYVF

```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCCTGCCCTGCCCCACCCAGGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTCTG
 ACC**ATG**GTCCCTGCCCTGGCTGTGGCTGCTTGTGTCTCCGTCCCCAGGCCTCTCCCAAGGC
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAATTTCCCTTTATACC
 TGACCAAGTTGCCGCTGCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCA
 GGCAAGGCACTGAGGGGCCATTGTCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG
 GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC
 CTTCCTTCTACCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACCTCGGATCTTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAAGGCCACTG
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCTATACCCGCACCACATGGCCAGGTACACTGGAGTGGGGGTGATGT
 GCATATCACCTGGAGACCATCCCCGGGACCTTTGAAGTGAATGTCAGAGGGGAAACCTCT
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTCCCATGGCGAGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
 TGACAACGTGCCCTATCTGCCCTCCCCGTGACCCACAGCTACGATCCCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGACTAGACTGTGACAGAGGATGAGATGCCCCGGCTCCCCCAATTCC
 CACGTTGTATCAGTCTCTGAGCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
 GGTGGACCCCACTTACGACGTGTGACGCTGGGGGTGCTCCCACTCCAGCAGGCCAGACA
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGCTTTCAGCAGCACGTGT
 GAAGTGAAGTCGCACTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGAT
 TGGGCCATATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCAGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGGCTGGATTGGGAGCCAGACTCTGGCGATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCAAGTTGGACCAGGAGAGCTACGAGGCCATGTCCTCCCATCAGTGGCCCC
 AGCCGGCTCTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCT
 CCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC
 GCCCAGTCCCTCGAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCCAGGA
 TACAGCCCTGACTCTTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC
 TTCACCTTGGTCCCAACCCACCGTGCAACGGGATTGGCGCTCCAGACTCTCAATGGTTT
 CCATGCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCAGTGAACACATAATCCCCGTGG
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGCTCGCTGCAAC
 GTGGAGGGGCGATGCATGCCAAGGTGGGCGCATGAAGGGATGCCCAAGAGCTGTGCGG
 AGTGGGCGATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCCTCATCCTCATTTTACCC
 ACTGACCATTGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG
 ACTGTG**TGA**ATGGCCAGGCAGCTCTAGCTGGGAGCTTGCCCTCCTGAGTCTCTGAGTCCC
 CTGGGAGAGAGCCCAAGCACCCTAAGTCCAGCAGGGGACAGGACAGATAGAGGCCCTCCAT
 CTGCCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGTCTGCAGAGCTGGACACCAAC
 TTTATGAGCTGCCATGGGAGTGTCTCAAATGTCAAGGTGTTTGCCCAATATAAAGCCCCA
 GAGAATCGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPaelSVEVPENYGGNFPLYLTkLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGfLLVTRALDREEQAeyQLQVTLEMQDGHVLWGPPVLVHVkdENDQVP
 HfSQAIYRARLSRGTRPGIPfLFLEASDRDEPGTANSDLRfHILSQAPAQPSpDMfQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSIIESTWVSLEPIHLAE
 NLKVLYPHHMAQVHWSSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPLELHVLVMDENDNVPICPPrDPTVSIPELSPPGTEVTRLsAEDADAPGSPNSH
 VVYQLLSPEPEDGVEGRAfQVDPTSGSVTLGVLPfLRAGQNILLVLAMDLAGAEGGfSSTCE
 VEVAVTDINDHAPEfITSQIGPISLPEDVEPGTLVAMLTaIDADLEfAFRLMDfAIERGdTE
 GTfGLDWEpDSGHVRLRLCKNLSYEAAPsHEVVVVVQSVAKLVGPGPGATATVTVLVERV
 MPPPKLDQESYEASVPISAPAGSfLLTIQPSDPISRTLRFSLVNDSEGWLcIEKFSGEVHTA
 QSLQGAQPGDtyTVLVEAQDTALTlAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGPnPTVQRDWRLQTLNGSHAYLTlALHWVEPREHIIPVVVSHNAQMWQLLVRVIVCRcnV
 EGQCMRKVGRMKGMPTKLSAVGILVGTlVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAATCTCCCTCCTCCT
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCAGTCTGCAGGCATTTAAATCCTTCTCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
 AGATGATGAAATGCAACACAAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG
 CTTACCATTTCCCTGGGAAGCTATTTACCACGAGATGGACAACATTGCCGACGACTTTCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTGAAAACCGGCCGATGTATGTACTGAAGTT
 CAGCACTGGGAAAGGCGTAGAGCGGCCGGCCGTTTGGCTGAATGCAGGCATCCATTCCCGAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTGTGTGCTGTGGCCAATCC
 TGATGGATATGTGTACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC
 CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTCAGGAAG
 GGAGCCAGCGACAACCCTTGCTCCGAAGTGACCATGGACCCACGCCAATTCGGAAGTGGGA
 GGTGAAATCAGTGGTAGATTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCCGAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCATCAGTCC
 GAGGAATCGACAAGGTGGCGAGGCTTGGGCCAAAGCTCTGGCTTCTGTGTGCGGCCTGTA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAACGGCATCAAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC
 TTCCTCTGCCAGCTAACAGATCATCCCACCTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTACTAGCGCATGGCTCTGCTCTGCTACATTTAT
 TTGTACCCACAGCTGCACGCATGAGGCAATTTGTTAAAGGAGCTCTTCCCTACCTGTGTGAG
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGTCCTGGCGGTGTCCCTGCAAGAACTGGTTCGCCAGCCTGCTCAATTTTGGTCCTG
 CTGTTTTTGATGAGCCTTTTGTCTGTTTTCTCCTCCACCCTGCTGGCTGGGCGGCTGCACCT
 AGCATCACCCCTTCTGGGTGGCATGTCTCTCTACCTCATTTTTAGAAACAAAGAACATC
 TGAGATGATTCTTACCCCTACCCATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT
 GTGGGAGACACCCTTGCTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTCCTTAATTTT
 TCGCAGTCTTCTCGGAAAATATTTTCTTTGAGCAGCAAACTTGTAGGGATCATAGTGAAG
 GTCTCTCCCTCCCTCTCTCTGTTTTTTTTTTTTTTTTTTGAGACAGATTTTGCTCTGTGGCC
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAAGCA
 ATTCTCTGCTCAGCCTCTTGTAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA
 ATTTTGTGTTTTTGTAGTAGACAGGGTTTCTCCATGTTGGTCAGGTCAGCTCTCAAATCCCA
 ACCTCAGGTGATCTGCCCTCCTTGGCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
 TGCCGGGGCCCGTCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCCTTCAC
 TGTGCTGAGAATTTCTAGATACATACAGTTCTTACTCCTCTCTCCCTTTGTTTATTCAGGTG
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTGCAGGATGGTGAATTTATCCCATCTGTCTCAATGGGCTTACCTCCT
 CTTTGGCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCCTAAATCACTCAT
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTTGTGCTGTGGTGTATCCTGTGTT
 TCCTTGTCTCTGGTTTGT
 TCTGTCTATTTGTATCTCTGGACCACAGTTCTTAAGTAGAGCAAGAATTCATCAACCAAGCT
 GCCTCTGTGTTTCATTTCACTCAGCACGTACCATCTGTCCCTTTGTGTGTGTGTGTGTGT
 TGTGTTTTTTGCTTTTACCAACATGTCTGTAATCTTAACCTCCTGCCTAGGATTTGTACAA
 GCATCTGGTGTGCTCTTATAAGCCAATAAAATTTCAATGTGAAAAAATAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFRLSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRWLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFTQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDONLY

Signal peptide:

amino acids 1-16

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CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAGACATATTTTGTCCAAAATG
GCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTC
CCCGGCCAATGCCCCAGTGCATACCCCCGCCCTTCTCCACAAGAGCACCCCTGCCTCAC
AGGTGATATTCCCTCAACACCGACTTTGCCTTCGCCTATACCGCAGGCTGGTTTTGGAGACC
CCGAGTCAGAACATCTTCTTCTCCCTGTGAGTGTCTCCACTTCCCTGGCCATGCTCTCCCT
TGGGGCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTTCAACCTCACACACA
CACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTCACTGACTGTTCCGAGC
AAAGACCTGACCTTGAAGATGGGAAGTGCCCTCTTCGTCAAGAAGGAGCTGCAGTGCAGGC
AAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTTCTACAGATTTCTCCA
ACCCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAGCCCAAGGGAAGGTT
GTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCATGGTTCCTGGTGAATCACATTTTCTT
TAAAGCCAAGTGGGAGAAGCCCTTTACCTTGAATATACAAGAAAGAACTTCCCATTCCTTGG
TGGGCGAGCAGGTCACTGTGCAAGTCCCCATGATGCACCAGAAAGAGCAGTTTCGCTTTTGGG
GTGGATACAGAGCTGAACTGCTTTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTT
CTTTGTCTCCCTAGCAAGGGCAAGATGAGGCAACTGGAACAGGCCTTGTGAGCCAGAACAC
TGATAAAGTGGAGCCACTCACTCCAGAAAAGGTGGATAGAGGTGTTTCATCCCAGATTTTCC
ATTTCTGCCTCTACAATCTGGA AACCATCCTCCGAAGATGGGCATCCAAAATGCCTTTGA
CAAAAATGCTGATTTTTTCTGGAATTGCAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCC
ACAAGGCTGTGCTGGATGTGAGTGAAGAGGGCACTGAGGCCACAGCAGTACCACCACCAAG
TTCATAGTCCGATCGAAGGATGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCCT
GATGATGATTACAAATAAAGCCACAGACGGTATTCTCTTCTAGGGAAAGTGGAAATCCCA
CTAAATCCTAGTGGGAAATGGCCTGTAACTGATGGCAGATTGCTAATGCACAAGAAATAA
CAAACCACATCCTCTTTCTGTTCTGAGGGTGCATTTGACCCAGTGGAGCTGGATTTCGCTG
GCAGGGATGCCACTTCCAAGGCTCAATCACCAAACCATCAACAGGGACCCAGTCACAAGCC
AACACCCATTAAACCCAGTCAGTGCCTTTTTCCACAATTCTCCAGGTAAGTCTTATG
GGATGTTGCTGGGTACCATATTTCCATTCTTTGGGGCTCCAGGAATGGAAATACGCCAAC
CCAGGTATTAGGCACCTCTATTGCAGAAATACAATAACACATTCAATAAAACTAAAAATGAAT
TCAAAAAA
AAAAAA

FIGURE 136

MASYLYGVLFAVGLCAP IYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESA IHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEA EVFSTDFSNPSIAQARINSHVKKKTQ GK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMHQKEQFAF
GVDTELNCFVLQMDYKGDVAFFVFLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGI AKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

FIGURE 137

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
 SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESTTSSGASTATNSE
 SSTPSSGASTVTNSGSSVTSSGASTATNSESTVSSRASTATNSESTLSSGASTATNSDSS
 TTSSGASTATNSESTTSSGASTATNSESTVSSRASTATNSESTTSSGASTATNSESTTSS
 SNGAGTATNSESTTSSGASTATNSDSSTVSSGASTATNSESTTSSGASTATNSESTTSS
 GASTATNSDSSTTSSGAGTATNSESTVSSGISTVTNSESTPSSGANTATNSESTTSSGA
 NTATNSESTVSSGASTATNSESTTSSGVSTATNSESTTSSGASTATNSDSSSTSSEAST
 ATNSESTVSSGISTVTNSESTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
 SEAKPGGSLVPWEIFLITLVSVVAAGLFLAGLFFCVRNLSLSLNTFNTAVYHPHGLNHGLGP
 GPGGNHGAPHRPRWSPNWFWRPVS SIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAAATCACGC
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTGCCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
CTGCTGGACAGGCCGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCAACCATGCTGCTGGCCAGGCCGGAAGGAGC
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCTTAAACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGAC
ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGTTGTACTG
GGATTTGTGAATAAACTTGATACACCA

FIGURE 140

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVKGALDGINSGITHAG
REVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

1-25
26-35
36-45
46-55
56-65
66-75
76-85
86-95
96-105
106-115
116-125
126-135
136-145
146-155
156-165
166-175
176-185
186-195
196-205
206-215
216-225
226-235
236-245
246-255

FIGURE 141

FIGURE 142

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962

><subunit 1 of 1, 837 aa, 1 stop

><MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSLWAAPWGALPPRPPLLLLLLLLLLLLLPPPPPTWALSPRISLPLGSEERPFRLR
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSEFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFQGNDFPAISRSQSLRPPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFLLMDGQVR
SRMLLLQPQARYQRVAVHRVPGLLHHTYDVLFLGTGDGRLLHKAHSVGPVRVHIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSlyQP
QLATRPWIQDIEGASAKDLCSASSVSPSFVPTGEKPCEQVQFQPNVTNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLVLVGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVII STSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECA SVHPKTCPVVLPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSESEKR
PLSIQDSFVEVSPVCPRPVRRLGSEIRDSVV

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGCGCGCGCGCGCTACGAAGAGGACGGGACAGGCGCGGTGCGAACC
 CGCCAGCCGCGGAGGACCGGGCAGGGCGGGACGGAGCCCGGACTCTGCTGCCGCCGCCGTCTGCGCGGTG
 TGC CGCCGCCGCTCCCCGCGCGAGCGGGAGGACCGCGCCACCTTCTGCCCGAGCCGCCGTACGCCGCGC
 CGGGCATGGTCCCTCTTAAGGGCGCAGGCCGCGCGCGCGGGCGGGTGTGCGGAACAAGCGCCGCGCGGGG
 CCTCGCGGCGGCTCGGGGCGCGCATGGCGCGCGCGGGCCCGCGCGCGCGCGCGCTGCCGGGCGGGGCTCG
 CGCGCTAGGGCGGGCTGGCTCCGTGGCGGGGCGAGCGGGCTGAGGCGCGCGCGCTCTGCGCGCGGGCGG
 GCGCGCGGGCGCGGGCGGGCGGGCGGGCAGGGCGCGCGCGCGCGCGCGCGCTGCGCGCGGGCGGGCG
 TGCTTCGGGCTTCGTCTGGGCTTCGTCTGGCTCGCGGCTCGTCTGCCCGGGCTTCGAGACTGAAGCGAGCGG
 GCCACGGCGCCGCGCCAGGCCCGAGGGCTGCCGGTCCGGGACGGCGCGCGCTTCCAGGCGCGCGGGCGCGCG
 GCGATGCGCGGGGCGCGAGCTTGGCCCGCGGGCTCGGACCCAGATGGCGGCGCGCGCGCAGAGAACTTTCTCT
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCGCTGGCGCGCTACAGAACATGGTCCAAGACAA
 TTCTCGGGAAGTTCAGTTCTTCTCAAGTGAGGGTTCTGACACATCTGTACCAATTCAGTAGTGCCACTACGGG
 GTGTGGAGCACTCTACCCGCCCCAGAGAAGTCTTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA
 AGTATGAATGGTTTATGAGGCGAGTATGACGTGTACATCAAAAGGACCGTCTGGAGAACTCTGAGGAGTT
 TGAACACGACCGAGCCCTCTTTCTTGGCGAGACAGGCTTGGGACCCAGGAAGAAATGGGAAAATGGCCCTGG
 AGCCTGGTGAGAACTTCTGCATGGGGGGGCTTGGCGTGATCATGAGCGGGAGGTGCTTCGGAGAAATGTCGCCG
 ACATTGGCAAGTGTCTCGGGAGATGTACACCACCCATGAGGACGTGGAGTGGGAAGGTGTGTCCGAGGTGTG
 CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCGAGCTTTTATGAGAAATTCAGCGCAGAAACAAAAGGGT
 ACATTAGAGATCTCCATAACAGTAAATTCACCAAGCATATCAATTACACCCCAACAAAACCCACCTACAGT
 ACAGGCTCCACAGCTACATGCTGAGCGCAAGATATCCGAGCTCCGCCATCGCACATACAGCTGCACCGCGAAA
 TTGTCTGATGAGCAAATACAGCAACACAGAAATTCATAAAGAGGACCTCGAGCTGGGAATCCCTCCCTCTTCA
 TGAGGTTTCAGCCCGCGCAGGAGAGGAGATCTGGAATGGGAGTTTCTGACTGGAAATACTTGTATTCGGCAG
 TTGACGGCCAGCCCTCGAAGAGAAATGGACTCCGCCAGAGGGAAGCTTGGACGACATTTGTACTCAGGTCA
 TGGAGATGATCAATGCCACGCCAAGACCAGAGGGCGCATCATTTGACTTCAAGAGATCCAGTACGGCTACCCG
 GGGTGAACCCCTGATGAGGCTGATGACTCTGGACTCTGCTCTGTCTGTAACAAAGCAACAAAGGAGAGAAA
 TGACGGTCCCTGTGAGGAGGCACGCGTATTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC
 TGGATGCACAAGATTGGCCAGAGAAATCAATCAGGAATCTGGATCCTTGCTCTTCTCTCAAACTCCCTGAAGA
 AGCTCGTCCCTTTTCAGTCCCTGGGTGGAAGGTGAGCACAAAGAACCCAAAGATAAAAAGATATAACACTACTGA
 TTCCTTTGTCTGGCGGTTTCGACATGTTTGTGAGATTTATGGGAAACTTTGAGAAGACGTGTCTTATCCCAATC
 AGAAGCTCAAGCTCGTGTTCTGCTTTTCAATTCTGACTCCAACCTGACAAGGCCAAACAAAGTTGAATGATGA
 GAGATTACCGCATTAAGTACCTAAAGCCGACATGCAGATTTTGCTCTGTCTCGAGAGTTTTCAGAGCCCTGG
 CCCTGGAAGTAGGATCTCCAGTTTAAACAATGAATCTTGTCTTCTTCTGACCGAGCTCGACTCTGTGTTTACTA
 CAGAATTCCTTCAGCGATGTGCAGCAAAATACAGTTCTGGGCGCAACAAATATATTTTCAATCATCTTCAGCCAGT
 ATGACCCAAAGATTGTTTATAGTGGGAAAGTCCAGTGACAAACATTTTGGCTTTTCACTCAGAAAACCTGGCTCT
 GGAGAAACTATGGTTTGGCATCACGTGATTTTATAAGGAGATCTTGTCCGAGTGGGTGGGCTTGATGTTTCCA
 TCCAAGGCTGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGAGGTTTGAAGACGTTTAGGAGCC
 AGGAAGTAGGAGTAGTCCAGCTCCACCATCTGTCTTTTGTATCCCAATCTGACCCCAACACAGTACAAATGT
 GCTTGGGGTCCAAAGCAGCTATTTGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAACAAATGATCCAA
 GTTACAGTAAAGCAGCAATAATTAATGGCTCAGTGAGCAGACGCTTAATGTCCAGCTTTGCTGGAAAAGACGTTTT
 TAATTAATCTAATTTATTTTCAAATTTTTTGTATGATCAGTTTTTGAAGTCCGTATACAGGATATATTTTAC
 AAGTGGTTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTCTGAACAAGAAGGTGATCAGTTTGGCTTTGAA
 CACATCTCTTGTGTAACATTATGTAGCAGACCTGCTTAACTTGACTTGAATGTACCTGATGAACAAAACCTTT
 TTTAAAAAATTTCTTTTGGAGCCCTTTGCTCCAGTCTATGGCAGAAAGGTGAACATCTCTGCAAAAGTAT
 TATTGTAAACAAACACTGTAACTCTGGTAAATGTTCTGTTGTGATTGTTAAACATCCACAGATTCTACCTTTTGT
 GTTTGTGTTTTTTTTTCAATTTGTTTTAAAGCCATTTCTGTTCCAGTTGTAAGATAAGGAAATGTGATAATA
 GCTGTTTCAATATGTCTTCAGGAGAGCTTTCCAGAGTTGATCATTTTCTCTCATGTGACTCTGCTCAGTATGGC
 CAGTAGGTTTTTTGTTTGTGTTTTGTTTTGTTTTGTTTTGAGACGGAGTCTCAGCTGTGTACCGGCTGGAATG
 CAGTGGCGCAATTTTGGCTCACTTTAACTCCACTTCCCTGGTTCAGCAATTCCTCTGCTTGGCTCCCGAGT
 AGCTACAGTTACAGCGACACCAACACCGCCAGNAGTTTTTTGTATTTTATGATAGACGGGTTTCCACAT
 GCAGGCCAGCTGGCCAGCTAGTTTTTAAAGCAAGGGGCGTGGAAGAGGCACAGTGAAGTATGGGCTGTTCTCG
 TGGTAGTTCTTTCGCGCTAAATAGACCTCGCATTAATTTCAAGAAGGATTTGGCATTTTCTCTCTTGACCTT
 CTCTTTAAAGGGTAAAAATTAATGTTTGAATGACAAAGATGAATTTACAAATAATCTGATGACACAGACT
 GAAACATACACATACACCTTAACAAAAGTGGGGAAGAAATGATTTGGTTTTGTTCTCTTCACTCTGTCTG
 TGTATGTGGGTGGAGATGTTTTTCACTTTTCAATGCTTTTTGTTATCTCTTGTATCTGAAATACCTTTAA
 TTTATTTAATATCTGTGTGTGAGAGCTGCGCAATTTCTTGAGTACCTGTTAGTTAGTATTTTATGTGTATCGG
 GAGTGTGTTTAGTCTGTTTTATTGTCAGTAACCGATCTCCAAGGATTTCTTTTGGAAACGCTTTTTTCCCTCC

FIGURE 143B

TTAATTTTATATTCCTTACTGTTTACTAAATATTAAGTGTTCTTTGACAATTTGGTGCTCATGTGTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTGCCATTTAATACACGTCAATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTTGGAAAAATAAACCACTGAACAATATTTTCTATTGACTTTTCGAACCATTTTGTCTCAIT
ATTCCTGTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAA

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FIGURE 144

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRA GPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAA YRTWSKTIPGKVQFFSSEG
SDTSVPPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWWSYEMRQLFYENYEQNKKGYIRD LHSNLSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQRQREE
ILEWEFLTGYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMIN ANAKTRGRIIDFKEIQY
GYRRVNP MYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTF SKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVPPQLPGSKSEHKEPKDKKINILIP LSGRFD MFVRFMGNFEKTC
LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQIL PVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSPDNHFAFT
QKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEVDVLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
TTTCGGCCTTGAGGTTCCCAGCCTGGTGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
ACGGACGACGCCTTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCG
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
CAAGTTTTAGAGAACCCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC
TAACTCTCCAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
ACTTTCCTACAGGAGGCTTCACACCGAAATAGGAAAGAAAAACACACGAAAGTACCCC
ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
AAAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCTCAGCTCT
CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTTGAAAAGCACCCAGAGAGTTGGAATAAT
GATGACATTTTGAAAAAAATTTTAGATATTAATTACAAGTGCAACAGGCACCTTCTTAGTGA
CACCAGCAACCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
TTGCTCTAGCAGCAGCAGCAGACAATAAATAAAAACAATGTATAAGTCCCAGTTATTGCCA
GTAGGACGAACAAGTAATAAATTTGATGACATCGAAACTGTTATTAAACATGCTGTGTAATTC
TAGATCTAAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
AAAGTTTATTAAACAATAATATAAAAAATTTAAACCTACTTGATATTCATAACAAAGCTGA
TTTAAGCAAACGTCATTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA
ATTTTCATATGCACTAAAAACCTAATTTAAATAAAATTTTGGTTCAGGAAAAAA

FIGURE 146

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTPGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEOPYIENEPEPEPEPAAKQTEAPRMLPVVTESSSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIE TVINMLCNSRSKL
YEYLDIKCVPEMREKAATVFNTLKNMCRSRRTALLKVY

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
ACCTCCAATCATCCATCCACCCCTGCTGTCTGTTTTCATAGTGTGAGATCAACCCACA
GGAATATCCA**ATGG**CTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA
GTGGCAAGTCACTGGACCGGCAAGTTTGTCCAGGCCTGGTGGGGGAGGACGCCGTGTTCT
CCTGCTCCCTCTTTCCTGAGACCAGTGCAGAGGCTATGGAAGTGGGTTCTTCAGGAATCAG
TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
GTATCGAGGGGAAGTGTGAGTTTGTGAAGGACTCCATTGCAGGGGGCGTGCTCTCTAAGGC
TAAAAACATCACTCCCTCGGACATCGGCCTGTATGGTGCTGGTTCAGTTCAGATTAC
GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT
CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTTCCCCAGC
CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAATGCA
GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAAATGCTGGGAGCAT
ATTGTGTTCCATCCACCTTGTCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
AGACGTTTTTCCAGCCCTCACTTGGCGCTGGCTTCTATTTTACTCGGGTACTCTGTGGT
GCCCTGTGTGGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAGGGAAAAATCCA
GGCGAACTGGAGTGGAGAAAGCACGAGCAGGACAGGCAAGTGTGAGAGACGCCCGGAAACAG
CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTTCTGATCTGAAA
ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA
GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTG
ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTAC
ATTCAATCCCCATTTTATCAGCCTCCCCCCAGCACCCCTCCTACACGATAGGGGTCTTCC
TGGAATATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCACTCCCTATTATTATACC
CTGCTGACATGTCACTTTGAAGGCTTGTGAGACCCCTATATCCAGCATGCGATGTATGACGA
GGAAAAAGGGGACTCCCATATTTCATATGTCCAGTGTCTGGGGAT**AG**GACAGAGAAGACCTG
CTTAAGGGGCCCCACCCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCCGACAGGTGGC
CCAGCTTCTCTCCGGAGCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTTAGGGAGC
TGAGGTTCTTCTGCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT
TGGCCTGACCCGTGTGGGAGTCAGAAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
CATTAGGTTTAGTTTTGTGAAAACCTCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTCGCCTCACAGGTGAAGATTAAAGAGA
CAACGAATGTGAATCATGCTTGCAGGTTTGGGGCACAGTGTTTGTCAATGATGTGTTTTTA
TATTATACATTTTCCCACCATAAACTCTGTTTGTCTTATCCACATTAATTTACTTTTCTCTA
TACCAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG
GAGGTAGGATTTTCTACTGATTCTATAAGCCCAGCATTACCTGATACCAAAACCAGGCAAG
AAAACAGAAGAAGGAAGGAAGGAAAACTACAGGTCCATATCCCTCATTAAACACAGACAAAAA
TTCTAAATAAAATTTTAAACAAATTAACCTAAACATATATTTAAAGATGATATATACTACT
CAGTGTGGTTTGTCCACAAATGCAGAGTTGGTTTAAATATTTAAATATCAACCAGTGTAATT
CAGCACATTAAATAAGTAAAAAAGAAAACCATAAAAA

FIGURE 148

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRRFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSRWLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFGAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAGAGTTTGTGTGGGAACCCCTGGGTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCAGTGTTCATTATGTGAGATATAATCAAAGAAGACCTACAA
 TTACTATAGCACATTGTCAATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA
 TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAAATGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGTGCTCACTGTTTTACAACATATAA
 GAACCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT
 CTGTCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAAATCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCCTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCCAACAAG
 CCTGGTGTTTATACTAGAGTTACGGCCTTGGCGGACTGGATTACTTCAAAAACCTGGTATCTATA
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGAC
 TTGTTGACATAAAATTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCCTC
 AGCTCCTCTCATTTAGCAAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGTGTTTTTCTTAGT
 GGAATATTAGAAATGATCATATTATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAATAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTCATTTCCAACAACCTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAACCTTCATGCAATGTACTTGTTCTAAGCAAATTAAGCAAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSFPVPYTNVHRVCLPDASYEFQPGDV
MEVTFGFGALKNDGYSQNHRLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWIYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACTGACAGCA
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTGAGCTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
 CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGGCCCTCAAGACTTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCCCTTGGCCGGCTGTCCCTGCGACTACGACCCTGC
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCCTGCCTGTGCCC
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCCTCCACTACTGG
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG
 CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTTATGTGCTTGCCTAGTGGCCGCTA
 ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
 CTTGCCCTTCGGGCCCTTGACGCCGCTTGCGGTGCCGCCAACCCCCGACTCTGGTCCACGC
 GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGGATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGAGGGGCGCTCTGA
 AAGGGGCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG
 GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
 GCTCCAGGGCCACGGCGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT
 GGCGCTTGTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTAAAAA
 AGCGGCCAGATAATAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

FIGURE 152

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLDGSEA
AQKGPPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHAVGVGTALALLSAAALVWHFCLRDWRWGCPRRAAARAAGAL
```

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTC
 CTGCCCGCATGAGCCCCCGCGTCCCGACTATCCCAGGCGGGCGTGGGGACCCGGG
 CCCAGCGCGGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC
 TTCTCCCTTACGGGGCTCACA**ATGG**CCAGAGAAGATTCCGTGAAGTGCTGCGCTGCCGTGCT
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCATCAGTGTGTTGGCAGTTCCTGCTTGGGA
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACAGAGGGTAGAGGAAGCAGCT
 ATTTTGACTTACTTTCTGTGGTTTCATCCGGTCATGATGCTGTTTGTCTGTTCCCTTATCAT
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAGAAATCTGTTGCTTCTTGCATGGTACT
 TTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG
 GAACCTTATGGTTCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCCGTGGCTTACTCATGCTTGAATTTTTTTCAGAGAGAGTTTAAGT
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGAT
 TCCTGCTGTGTTAGAGAATTC**CC**AGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTGAGAGGAACCAAAACAACCTGC
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTC
 CTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTTA**TAA**AAAGAAATGTCACAGAAGAAAACCAAAACTGTTTTATTGGACTGTGTAATT
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAATGTTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTTAAAAAGAGGATGGAAAAGTTTCATGTCTAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTGGAGCAGCATGGTTTGATTAGCATTTTC
 CGCATCCATGCAACCGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT
 CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAACTACTAATA
 ACTTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTC
 AATATTGGTGACTACCTAAATGTGATTTTGTCTGGTTACTAAATATTCTTACCCTTAAAA
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAA
 TCTGTATAATTCAAGTCGATTTCACTTCTGATAATGTTAAGAATAACCATATGAAAAGGAAA
 ATTTGTCCTGTATAGCATCATATTTTTAGCCTTTCTGTTAATAAAGCTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTA
 CCAGTGTGATACATAGGAATCATTATTAGAAATGTAGTCTGGCTTTTAGGAAGTATTAATAA
 GAAAATTTGCACATAACTTAGTTGATTGACAAAGGACTTGATGCTGTTTTTCTCCCAATG
 AAGACTCTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCAACAAGAA
 GCAATAGTCTCCAAGTCAATATAAATCTACAGAAAATAGTGTTCTTTTCTCCAGAAAAAT
 GCTTGTGAGAAATCATTAACACATGTGACAATTTAGAGATCTTTGTTTTATTTCACTGATTA
 ATATACTGTGGCAAATTACACAGATTATAAATTTTTTACAAGAGTATAGTATATTTATTT
 GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTATTTCTCAGAATATGGAA
 AGAAAATTAATAATGTGCAATAAATATTTTCTAGAGAGTAA

FIGURE 154

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLALLAWYFGSLLVIFCVELACGVWTYEQELMVFPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPQTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCC
 TGCACTCGGGCTCCTTCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGG
 TGATTCTGGATAAAATACTACTTCCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCAGAGGGCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA
 TGTGTGTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACCAAGTGGGCCCTGTC
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCCGT
 GTGGTGGGTGGGGAGGAGGCCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACT
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCAA
 AGACAATGACATCGCCCTCATGAAGCTGCAGTCCCCTCACTTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
 GGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCCCAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTGTAATGCTGCTGCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCTCTG
 CCCTGCCCACTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC
 CTCTGCCACAGCCTCAGCATTCTTGGAGCAGCAAAGGCCTCAATTCTGTAAGAGACCC
 TCGCAGCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
 AGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACTTCCCACACTACTGAATGGAAGCAGGCTGTCTGTAAAAGCCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGGCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA
 CTAGAGCAAGAAACAGTTGTAATATAAATGCACTGCCCTACTGTTGGTATGACTACCGTT
 ACCTACTGTTGTTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACTCT
 CTGGCAAAAAAAAAAA

FIGURE 156

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVLIKVILDKYYF
 LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
 SACFDNFTEALAEACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSL
 HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWLTAAHCFRKHTDV
 FNWKVRAGSDKLGSFPLAVAKIIIIIEFNPMYPKDNIDIALMKLQFPLTFSGTVRPICLPFFD
 EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
 GGVDTCCGDSGGPLMYQSDQWHVVGVISWGYCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCAGTGAAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAACCGCAGCGGCATCCCAGGCTCCAG
AGCTCCCTGGTGACAGTCTGTGGCTGAGC**ATGG**CCCTCCCAGCCCTGGGCTGGACCCCTGGAGCCTCCTGGGCC
TTTTCTCTTCCCACTGCTTCAGTGTCTGCTGCCGACGACAGCCGCGGGGGAGGCGGGCAGGGGCCCATGCCCA
GGGTGAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACAGAGAGGGCTCCAGGATTTTGACA
CTCTGCTCCTGAGTGGTGATGGAAATACCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGATATCCAGG
ATCCAGGGGTCCTCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA
AGAAGAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTCTCTGGTTCTTACAAATGTACCCATCTCTACA
CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTAACCTTCATTGAACCTTCAAGATTCTACCTGTTGCCATCTCGG
AGGACAAGGTCTATGGAGGGAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG
GGATGCTCTATTCTGGTACTATGAACAACCTTCCTGGGCAGTGAGCCCATCTGATGCGCACACTGGGATCCAGC
CTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGGCAGCCATCCCTTCGACCC
AGGTGCTGTACTTCTTTCTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG
CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGC
TGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTATCCGCCAGCGGTCTGCTCCCCGCCGATTCTCCCA
CAGCTCCCCACATCTACGAGTCTTCACTCCAGTGGCAGGTTGGCGGACAGGAGCTCTGCGGTTTGTGCT
TCTCTCTCTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA
CTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCTGTGATAAGGCCCTGACCT
TCTATGAAGGACCATTTCTGATGGATGAGCAAGTGGTGGGAGCGCCCTGCTGGTGAATCTGGCGTGGAGTATA
CACGGCTTCAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCAACACAG
GGTGCCTCACAGGCTGTGGTAAGTGGGACAGCAGTGCTCATCTGGTGAAGAGATTGAGTGTCTCCCTGACC
CTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTGTTGAGGCTTCTCAGGAGGTGTCTGGA
GGGTGCCCGAGGCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGCTTGGCCGGGACCCCACTGTGCT
GGGACCTGAGTCCGACCACTGTTGGCTCCTGTCTGCCCAACCTGCTGTGGAAGCTGGAAGCATGAGAGGGGG
GGAACCCAGAGTGGGCATGTGCCAGTGGCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCGCAATCATTA
AAGAAGTCTGGCTGTCCCCAATCCATCCTGGAGTCCCTGCCCAACCTGTGAGCTTGGCTCTTATTATT
GGAGTCATGGCCAGCAGCAGTCCAGAGCCTCTTCCATGTCTACAAATGGTTCCTCTTGTGATAGTGACGG
ATGGAGTTGGGGTCTCTACAGTGTGGGCACTGAGAATGGCTTTTATACCCCTGTGATCTCTACTGGGTGG
ACAGCCAGGACAGACCTGGCCCTGGATCTGAACTGGCAGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA
CCAGGGTCAGTGGTGGGCGCCCTGGTGGCCAGCAGTCTACTGGCCCACTTTGTCACTGTCACTGTCTCT
TTGCCCTTAGTGCTTTCAGGAGCCCTCATCATCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGCAAGG
TTCAGGGCTGTGAGACCTGCGCCCTGGGAGAGGGCCCCGTAAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG
AATGCAGGACCTCTGCCAGTGTGTGGACGCTGACAAACAACCTGCCTAGGCACTGAGGTAGCT**TAA**ACTCTAGGCA
CAGGCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGCTGGGCGGCCAAGCACAGCCCTGACTAGGATGACAG
CAGCACAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTGTGCATCACTGATGACACTCAGCAGGGTG
ATGCACAGCAGTCTGCCCTCCCTATGGGACTCCCTTACCAAGCACATGAGCTCTCTAACAGGTGGGGGCTAC
CCCAGACCTGTCTCACTGATATTGAAGAACCTGGAGAGGATCTTCAGTCTTGCCCATTCAGGGACCCCTC
CAGAAACAGAGTGTTCAGAGACCTCAAAAACCTGCCTGTCCAGGACCCCTATGGTAATGAACACCAACATC
TAAACAATCATATGCTAACATGCCACTCCTGGAACTCCACTCTGAAGCTGCCGCTTTGGACCAACAACCTCCCT
TCTCCAGGGTCAGCAGGATCTGCTCCCTCCTGCTTCCCTTACCAGTGTGCACCGCTGACTCCAGGAAGTCT
TTTCTGAAGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGCGAGACTGTGATCCCTTCTGCCCTGGCAGATGG
CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCTTCACTCTCCCCCTCCCTTTCTCTTGT
TTTGGGATTCAGAAAACTGCTGTGACAGACTGTTTATTTTATTAATAAATATAGGCTTTAAAAAA

FIGURE 158

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGQGPMRVRYYAGDERRALSFFHQKGLQ
DFDTLLLSGSGNTLYVGAREAILALDIQDFGVPRLLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFIMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLM
YLGTTTGSLSHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAPPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFLVLVSGALIIILVASPLRALRARGKVQCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGAA
 TGAGC**ATG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCTCTCCCTGGGGTCTGCTC
 TCAGAGGCTGCCAAATCCTGACATATCTACAGTAGTGGAGCCATTATCTACTGATGGA
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCCCATGCTTAACCCAAAAAGAG
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAGAACTTTAGG
 TGGCAGAGGAAAATTTGAAACCTTATTAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAACTTCGACATGGTGATA
 GTTGAAACTTTTGACTACTGTCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC
 CATTCTTTCCACTTCATTGGGCTCTTTGGAATTTGGGCTACCAATCCCCCTGTCTTATGTTT
 CAGTATTCGGTTCTTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATCGAGTCTACATTTGACAACACCATCAA
 GGAACATTTTACAGAAGGCTTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GGTTTCATTAACCTCTGACTTTGCCTTTGATTTTGTCTCGACCTCTGCTTCCCAACACTGTTTAT
 GTTGGAGGCTTGATGGAAAAACCTATTAACCAGTACCACAAGACTTGGGAGACTTCATTGTC
 CAAGTTTGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCTAGA
 ATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGTCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCAAGTGTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTTGGA
 CTGGCTTCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCACCACAGCG
 GGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTAGTT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCCGGCGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAG
 CGGCTGGTGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCAGCCACCTCAAGCCCTA
 TGTCTTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTTCTGCTGGGGC
 TCACTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTCGCT
 GGGGCCAGAAAGGTGAAGGAGACA**TAA**GGCCAGGTGACGCTTGGCGGGTCTGTTTGGTGG
 GCGATGTCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC
 TAGTTATCTCCTGTTTTCTGAAGAACAGGAAAAATGGCCAAAAATCATCTTTCCACTTGC
 TAATTTTGTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT
 CTGTCTCCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG
 GACCACTGACCTCAGATTTCCAGCCTTAAATCCACCTTCTTCTCATGCGCTCTCCGAA
 TCACACCTTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCTGCCCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACCTTGCATATTCCTTCAGTTTCTGTTT
 TGTCTTCCCATATTTCTCTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTACAGGGC
 CGGACACAGGCTCACAGGTTCCACATTTGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCT
 TCTTGGCTGAGCAGGCTGAGAGCTGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACA
 GCGTTATCTCTCCCCAACCTCACTAA

FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPVLLSEAAKILTIISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPF
FMPDFKKEEKSYQVISWLAPEHDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAEWLF
INSDFAFDFAFPELLPNTVYVGGLMKPKVPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAPHLPGQVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFTVTHGGQ
NSIMEAIIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPWHEQYLFDFVFVLLGLT
LGTWLWLCGKLLGMAVWVWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTCACACCCGTCACACACACATACCATTGTT
 CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTCAGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAAGAGGGGCAGA
 AGACCGGGGCACTTGTGGTTGCAGAGCCCTCAGCC**CATG**TGGGAGCCAAAGCCACACTGGC
 TACCAGTCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGGCC
 GGGTGGGCCAGGAGGGGTACAGGCCGTCTGCTGGAGGGGAGTGCCCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTCAGGGGGGCCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
 GAGTGGCATTGCTGCGGTCGGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACCAGGTCTCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCTGTCCGGGTGTCTACAGCTTCCGGTTCATGTGGTGAAGG
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCTCAGCC
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACAGCTCTGTGCTACTGCCCTTGGC
 CCTGGGGACCGAGTGTCTGCGCCTGCGTCGGGGGAATCTACTGGTGGTTGGAATACT
 CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCT**TGA**GGACCCAAAGTCTTCAAGCACAAGAAT
 CCAGCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAGTTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCACCCACCCACCCCGAGTTACC
 CTCCAGCCACCTGCTGCATCTGTTCTGCTGACGCCCTAGGATCAGGGCAAGGTTTGGA
 AGAAGGAAGATCTGCACTACTTTGCGGCCCTCTGCTCCTCCGGTTCCCCACCCAGCTTCT
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCAG
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC
 TCAGCCAGCACCGCTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCTGGAGTCTGTGGCTGGTAGGAAGGAAGGAGGGTGATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCTTCTATGTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC
 CTTTGAAGTTTGAACTTTAGTCCCTCCACACTGACTGCTGCCTCCTTCTCTCCAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCATATCTCTCTTCTCTCTGAT
 CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCTATTACCTGGGATTCCATGATTCACTCTT
 CAGACCTCTCTGCCAGTATGCTAAACCCCTCCCTCTCTCTTCTTATCCCGCTGTCCATT
 GGCCACGCTGGATGAATCTATCAATAAAACAACCTAGAGAATGGTGGTCACTGAGACACTAT
 AGAATTACTAAGGAGAGATGCCTCTGGAGTTTGGATCGGGTGTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAAATAATATCAAACCTGTATACTAAAATTAATAA

FIGURE 162

></usr/seqcb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECLEVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL

Signal peptide:

amino acids 1-32

FIGURE 163

FIGURE 164

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVFDWNTPKKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLSMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSPKITTVVGEPI TIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-
245, 318-323, 378-383

FIGURE 165

GGGCGGCGGGATGGGGGCGGGGCGGGCGCGCACTCGTGAAGGCCCGACGCAGGGCCGGGCGGGCCCA
GGGCGGAGGAGCGCGGCGGCGAGAGCGGGGCCGAGGCGACGCCGGGACGCCCGCGACGAGCAGGTGGCG
GGCGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGCGAGCTGTCCCACTGGCTCTGCTGACCTTGTGCCTTGGGA
CGGCTGTCTCAGCAGAGGGGCCGTGACCCCGCTCCTGAGCAGCGCCATGGGCTGTGTGGCCTTCTGAAAGACCCA
GTTTGTGCTGCACCTGCTGGTTCGGCTTTGTCTTGTGGTGGTGGTGTGCTCACTCAACTTCGCTCCAGCTGTGCAC
GCTGGCGCTCTGGCGGTTCAGCAAGCAGCTCTACCGCCGCTCACTGCCGCTCGCCTACTCACTCTGGAGCCA
ACTGGTCATGCTGCTGGAGTGGTGGTCTGCGACGGAGTGACACTGTTACGAGCACGGCCACGGTAGAGCGCTT
TGGGAAGGAGCAGCAGTCATCATCTCAACCACAACCTCGAGATCGACTTCCTCTGTGGGTGGACCATGTGTGA
GCGCTTCGGAGTGTGGGGAGCTCCAAGTCTCTGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGGCTGGAC
GTGGTACTTTCGGAGATTGTGTCTGCAAGCGGAAGTGGGAGGAGACCGGACACCGTGTGGAAGGCTGAG
GCGCTGTGGACTACCCGAGTACATGTGGTTTCTCCTGTACTGCGAGGGGACGCGCTTCACGGAGACCAAGCA
CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCTGTCTCAAGTACCACCTGCTGCCGCGGACAGGG
CTTACCACCGCAGTCAAGTGCCTCCGGGGACAGTCGCGAGCTGTCTATGATGTAACCTGAACCTCAGAGGAAA
CAAGAACCCTCCCTGTGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCCTCT
GGAAGACATCCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTTCATAAATGTACCAGGAGAGGACGCGCTCCA
GGAGATATATAATCAGAAGGCGATGTTTCCAGGGGAGCAGTTTAAGCCTGCCCGGAGGCGGTGGACCTCCTGAA
TCTCCTGTCTGGGCGGCAATTCTCCTGTCTCCCTCTTCAGTTTGTCTTGGGCGTCTTGGCCAGCGATCACC
TCTCCTGATCCTGACTTCTTGGGTTTGGGGAGCAGCTTCTTTGGAGTTCGCAGACTGATAGGAGAATCGCT
TGAACCTGGGAGGTGGAGATTGCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
CAGTCTCAAAAAAAAAAAAAAAGCAAAACCCAGAAATTCGGAGTTGAAGTGTGTAGTTACTGACATGAAAA
ATTCATAGAGGCTGAACAGCAGATTGTAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
TTTCAGGCTAATGAAAAAGAAATGAAGGAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCAACAAATCAA
CATATGCATGATGAGAGTCCCAAGAGGAGAGGAGAGAAAGGTCAGAAAGAAATGGCCACAAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCAT
AATCAAGTGTCAAATGACAAAGAAATCTTGAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGATCTTGTG
ATCAGATTAAACAGCTCATTTCTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCCAA
AACCTTCAACTGTAATTAATTGACTTTTGTAGTCTTAGATGGTCCGACCTCTTTGTCTTCAGGGACAGTTTTTCA
ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGAAGTGTAGGAAGGCTGTCTTTAGGCGGGCAGAGTGGC
TTACACCTGTAATCCAGCAGCTTTGGGAGGCCAGAGCGGTGGATCATTGGGGTGAAGCTGATCTCAAACTCCT
GAGTTCAGTGATCTGCCGCTCAGCCTCCAAAGTGTGTGATTGACGGGCTGAGCCACTGCGCTGGCCGGA
ATTTCTTTTTAAGGCTGAATGATGGGGGCCAGGCACGATGGCTCAGCGCTGTGATCCCAAGTACCTTGGATTGTA
AACATGCACCACCATGCTGGCTAATTTTGTATTTTGTAGTAGAGCTGTGAGCCAGGCTGGTCTCGATCTCCT
GACCTCAAGTGACCACTGCTCAGCTGCCAAAGTACTGGGATTACAGCGGTGAGCCACTGTGCTGGCCTTGA
GCATCTGTGATGTGCTATTGGCCATTGTGATATCTTCTATCTTCTTTGGGAAATGTCTGTTCAAGTCCCTTTG
CCTTTTTAAATTTTATTATTTATTTATTTATTTATTTGAGACAGGCTGTGTTCTGTGTGCCAGGCTGGAGTA
CAGTGGCAGAGCTTGGCTCACTGCAGCTCGACCTCCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTGT
AGCTGTATTTTTTGTATTTGTATTTGTAGCTGTAGTTTGTATTTTTTGTGGAGACAGCATTCACCATGA
TGCCAGGCTGGTCTTGAACCTCCTGAGTCAAGTGATCTGCCTGCTTCAGCCTCCCAAAGTGTGGGATTACAGA
CATGAGCCACTGCACCTGGCAAACTCCCAAAATTCACACACACACACAAAAAACCACTGATTCAAAATGGGCA
GAGGGGCCGGGTGTGGCCCAACTACCAGGAGACTGAAGTGGGAGGATCGCTTGGGATGAGAAGTCGAGGCTG
CAGTGAGTCGAGGTGTGCGAGTGCATTCCAGCCTGGACAACAGAGTGAGACCTGTCTC

FIGURE 166

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213

><subunit 1 of 1, 368 aa, 1 stop

><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTQFVLHLLVGFFVVSGLVINFVQLCTLALWPVSKQLYRRNLNCRLAYSLWSQLV
MLEWWWSCTECTLFSTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAAGLPVLKYHLLPRTKGFTTAVKCLRGTVAAYVDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLLILTLGLFVGAASFGVRRRLIGESLEPGRWRLQ

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTTAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCTCTGGGGCA
 GCCACCAGGCATATTCATCTTTGTGTGTGTCTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG
 GCTTACGCCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
 GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
 TTCTCTAACCTGGCATACCTGCTTAAAGCCTCTCAGGGCTTCTCTGTTCCTTAGGATCAA
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGT
 ACATGTGGTGTCTCTTGTCTGTTCCCTGTAATGTGGTATGCCATGGGGTCTTGCACAAGCCT
 TTCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC
 ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTTGTTTAAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCAAGCACTTGCCACTCAGTTGTA
 TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCTCAGAAATGCCAGCTCTGAGC
 TGCCTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
 CATGTTTATAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
 GATGGTGTAGGGCCAGCATTGTAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA
 TGCAGGTCTGATTCAGTAGGCCAGGTTGGGCATCTCTAACAAACTCCCACGTGATGCTGA
 TGCTGGTCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
 TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCAACATGGTGGAAACCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCACTGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAA

FIGURE 168

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRIHLCVCF SFALALGHFLLISLVGKGLSLSCGVGGRQAGRLRIPWVRR
EGKINFYTINGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
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Important features of the protein:**Signal peptide:**

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCTCAGCCTCCCAAGGTGCTGTGA
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTTCAGCAACTAAAAAGCCAC
AGGAGTTGAACTGCTAGGATTCTGACTTATGCTGTGGTGGCTAGTGTCTCTACTCTACCTAC
ATTAAAACTGTGTTTTTTTGTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT
CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTTCTACCCAC
ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGTA
GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTT
CATAGGCGATGGCTCCCACCTGCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT
CTAACCTTTTTCATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACCTCTGTCCCAAGG
AAGCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
TATGTGACAGGACTTGCATTCTCTGGAACATGAGGGAACCGCGAGGAAAGCAAAGTGGCA
GGGAAGGAACTTGTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGC
ATCGAGTCTCTGCAATTCAGTGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTTCCGCCCGATCCACGTACCAGCTGCTG
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCTCCTTCCCTC
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
GCTCAGTGTTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGTGTGCG
AACACGGAAATGCCCTCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
TCAAATGATCTCAAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAA
TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTTGGTGGCCTGTAATG
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTG
GCCAACATGTTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGTTGGT
GTGTGCCTGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
AAAAATAAAAAAGAATTATGGTTATTTGTAA

FIGURE 170

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVMFCSLVTSLSYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA

SPCWPLAGAVPSPPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

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FIGURE 171

GCGGGCCCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
 CCGCCGCCTCCTGCCCGCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCCTGCTTCCCCCGAGGACAGCCGCCTGTGG
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
 CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
 CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
 GCCCCCGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCAGGCGGAGCACAAAGATCGACCTCC
 GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGCGGGCGAGGCCGGCACCTTC
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGTCCGCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCTTCAGAGTCTGTGGCGCGGGAAGGTGCTGC
 AACCTCCGAAAGGGGACGTGGCGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
 GACGTCAGGGTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCTGGGAACCCAGGAATTGAC
 CCTGAGTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

FIGURE 172

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCCLLPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFGTGYSALALALAL
PADGRVVTCEVDAQPPPELGRPLWRQAEAEHKIDLR LKPALETLDDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRYVIS
LLPLGDGLTLAFKI

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

FIGURE 174

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYKPKNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDERD
VMAVTAVTATAASDRMESDSDSKSSDNSGLKRKTPALKMSVSKRARKASSDLQASVSPSE
EENSESSSESEKTSQDFTPEKKAAPRRRGLGGRKKKKAPSASDSDKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVSKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRRELEARRRREQEEELRRLEQEEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAQPVKVERTKRSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMEKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEKLAGEEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDEKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLDPRGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAANTTA
 ACACCTTTTGAAGAGAACATTTGTTTCATCATGAATGCTAATAAGAGATGAAGACCTTAAGCGCAGAGGCCAAGA
 TTTTCACCTTTTTCCTGCTTTGATGATGCTAAGCATGACCATGTTGTTCTTCCAGTCACTGGCAGCTTTGAAGCA
 AATATTCCCAAGACTCAAGCTTAACCTACAAAGACTTGCTGCTTTCAAAATAGCTGTATTCCCTTTTGGGTTTCATC
 AGAAGGACTGGATTTTCAAACCTCTTCTCTAGATGAGGAAAGAGGCCAGGCTGCTCTTGGGAGCCAAAGACACAT
 CTTTCTACTCAGTCTGGTTGCTTTTAAACAAAATTTTAAGAAAGATTTATGGCCTGCTGCAAGAGCAACGGGTGGA
 ATTATGTAAATTAGCTGGGAAGATGCCAATACAGAATGTGCAAAATTTTCATCAGAGTACTTCAGCCCTATACAAA
 AACTCACATATATGTGTGTGGAATCGGAGCATTTTCATCCAAATATGTGGGTATATTGATCTTGGAGTCTACAAAGGA
 GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTCCGATCCTCAGCAGCC
 TTTTGCCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCCCTTGGCAAGACATACTGCATT
 CACTCGATCCCTTGGGCCCTACTCATGACCACCACTACATCAGAACTGACATTTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTTTATGGAACCTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTCG
 TGAATCATCTCAAGAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT
 AGGAGGACAACGCAGCCTGATAAAACAAGTGGACCACTTTTCTAAGGCCAGACTGATTTGCTCAATTCTCGTAAG
 TGATGGGCGAGATACCTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCAAGAGATGAAGAAATCCTGT
 AGTATATGGAGTCTTTTACTACAAACAGCTCCACTTTCAAAGGCTCTGCTGTTTGTGTATAGCATGCTGCACAT
 CAGAGCAGCTTTTAAATGCTCCATATGCTCATAGGAAAGTGCGAGACCATCGTTGGGTGCGATGATGGGAGAT
 TCCCTTATCCACGGCTGCTGATCATGTCACAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA
 TGATGTCATCAGTTTCTATAAGCGGCAGCTCTGTGATGTATAAGTCCGTATACCAGTTTCAGGAGGACCAACGTT
 CAAGAGAAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCTATTTCAGAGAGATGGCCAGTACGA
 TTTAATGTTTCTTGGAAACAGACATTTGGAACCTCTCTCAAAGTTGTGAGCAATTTCAAAGGAAAAGTGGAAATATGGA
 AGAGGTAGTGCTGGAGGAGTTGACAGATATTTCAAGCACTCATCAATCATCTTGAACATGGAAATTTGCTCTGAAGCA
 GCAAAATTTGTACATTTGGTTCGCCAGATGGATTAGTTCAGCTCTCCTTGACACAGATGCGACACTTATGGGAAAGC
 TTGGCGAGACTGTTGTCTTGGCAGAGACCCCTACTGTGCTGGGATGGAATGATGCTCTCGATATGCTCCTCTAC
 TTCTAAAGGAGAGAGTGTGATCGCCCAAGATGTAAATATGGCGACCAATCAACCCAGTCTGGGAGCTGAGCAACAG
 CATTAGTCATGAACATGCTGATGAAAAGGTGATTTTGGCATTTGAATTTAACTCAAACCTTTTGGAAATGTATACCC
 TAAATCCCAACAAGCACTAATTAATGGTATATCCAGAGGTGAGGAGTGAACATGAGGAGTGAAGGCCGA
 TGAAGAAATCATCAAACGGAATATGGGCTACTGATTCGAAGTTTGCAGAAAGAGATTCTGGGATGATTAATCTG
 CAAAGGCCCAGGAGCACATTTTCATCCACACCACTAGTGAAGCTGACTTTGAATGTCAATTGAGAAATGAACAGATGGA
 AAATACCCAGAGGCGACAGCATGAGGAGGGGCGAGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAGA
 CTACATCCAATCCTTAGCAGCCCAAACTTCAGCCTCGACAGTACTGCGAACAGATGTGGCACAGGGAAGGCG
 GAGACAGAGAAACAAGGGGGGGCCAAAGTGAAGACACATGCGAGAAATGAAGAAGAAACGAATCGAAGACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGGCCAGCTAGTTTCTACTTAATTTAAAGAAAAGAAATTCCTTACC
 TATAAAACATTTGCTTCTGTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTGTCTAAGG
 CACAAGACAATAATCTGAATTAAGACAATATGTGATGAATATAAGAAAGGGCAAAAATTCATTGTAACAGGATTTT
 CCAAGACAATAATCTTGCAACAGCAAGATATAAGAAATTTATCCTAAAATATGGGGGTTTACAGTTGTAATATGTTTA
 TGTTTTGTAGTTTGGAAATTTATGTCATGTAATAGTTGAGCTAAGCAAGGCCGAATTTGATGATGATATAAGGT
 GCTTTATTTCCCTCGAATGTCATTAAGCATGGAATTTACCATGCAAGTTGTGCTATGTTCTTATGAACAGATATAT
 CATTCCTATTGAGAACAGCTACCTTGTGGTAGGGAATAAGAGGTGAGACACAAATTAAGACATCCCATTAATC
 AACGAAGCAATTTCTCAGTGAGCCATCTACTCTGAGGAATGGTATAGGAATTTGAGAGGTGCAATATTTCTTTT
 TGCCCTCTGGGTTTAAATTTAGTGTACTACAACTGATTTACTGAAGGCCATTAATGTTTCCCCGAGATTTCT
 ATTGACTAGTCAGGAGTAACAGGTTTCACAGAGAGAGTGGTGCTTAGTTAGTGTTTTGTAGAGTATATACTAA
 GCTCTACAGGACAGAAAGCTTAAATGATTAATTAATTAATGATATGGGAAATATTTTAAATAAGAAACAGGAAACAA
 TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTAGAGAGACAGAGGAAGACAGCCAT
 AAATCTCGGCTTTGGGGAACACTCATATCCCATGAAAAGGAGAACAACATACAAATTAAGTGAAGTAAATGTGA
 TGGAGCTCTTTTCACTAGGATATAAGTAGCTGCCAATTTGTAAATTCATCTGTTAAAAAAATCTAGATTATAACA
 AACTGCTAGCAAAATCTGAGGAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAACC
 AATGATATTTTCAGTATATATTTTCTCTTTTAAAAAATATTTATCATACTCTGATATATTTCTTTTACTGCTC
 CTTTATCTCTCCGTATATTTTGTGATTATATTTGAGTGAATAGGAGAAACATATATAACACACAGA
 GAAATTAAGAAATGACATTTCTGGGGAGTGGGGATATATATTTGTTGAATACAGAACAGTGTAAATTTTAAAC
 AACGGAAAGGTTAAATTAACCTTTTGCACATCTTCACTCAACCTTTCTCATGCTGAGTTAATCTGTTGTAATT
 GTAGTATTGTTTTGTAATTTAAACAATAAATAGCCTGCTACATGT

FIGURE 176

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKDLLLSNSCIPFL
GSSEGLDFQTL LLD EERGRLL LGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHHYIRTDISEHYWLNAGKFIGTFF
IPDTYNPDDDKIYFF FRESSQEGSTSDKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSAVCVYSMADIRAVFN GP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVVLEE
LQIFKHSSIIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNA
CSRYAPT SKRRARRQDVKYGDPITQCWDIEDSISHETADEKVI FGI EFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCYCKAQEHTFIHTIVKLTIN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRQRN
KGGPKWKHMQEMKKRNRHRRDLDELPRAVAT

Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCAACTGAGCTGGAAGCCGAGAGGTCATCCTGGAGCATGCCACCGCGGGGAGCAGA
 CAACTCCAGGTAAAGCTGGGAGCCAGACCTGAAGCTGTTTCTTCAGGAGCATGGTGTATTTCCGCCACCCAC
 CTCAGCACTTTGAGCCAGCAGGAGCTATGACGCTGTGTCTTCAGAGTGGGAGCAGAAGGCTGGCTGGCAGA
 GTGSCCTGGAGAAAGAGTTTACGCGCTTACACGACCCGAGCTGCCCTGACTACAGATCCAGAACCATGGGCATC
 GGGTGAGGTGGGGGGGACAGGTCGTATGTCACCTTCTTGTCTCAGCAAGAAGAGCTGACAGAGGGGATCTTGG
 AGCCATTGAGGTGTCTATGGAGCTACAGAGGGGAGGAAAGGTATTTAAAGTTAAAGTGTGGCACAATAGTTTAA
 GAGCACAGTTTTTTGAGCTAGACCCGATAGGTTCAAAATTTCTTCTGTGCTTCTTCTAGTTCTGTAGCCCCAGST
 AAGGGAGTGACTTAACCTTCTCGACTTCAATTTCCCTCATCACTAAAGTAGGGCCAATATAGCACCCCACTCAT
 AGGGAAGATTAATGACATAATGTATGTGATGCACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
 TATTTCCACCACCCCTGTTCTCTGCCTTCCCAACCAAGTACTGCAACGACTGGAGCAGAGGGCGGACAGGCTT
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCCGGGCACAGGTGAGCC
 AGCTGAAGGGGCTGCCCGGTGSCCTGCTGCAGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGCGGGCTCAGTGAGGCTCGGCTGTCCAGAGGGACCTCTCTC
 CAACCGCTGAGGATGCTCAGCTTTCCTGACTTTAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGACCTGCC
 CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACAGTGGTATTTGCTATCAGGCAGGGCGTGAGCATG
 AGCTGACATCAGGAGGCTGAGTGGCTGGAGGTCATAGAGGAGGAGATGCTGACGAATGGGTCAAGGCTCGGA
 ACCAGACCGCGAGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCAGAGGAGCGCC
 AAGCAGTGACAAATCCCTGCGGGCAGAGCCCAAGCATTCCTGGCAGAGGCCCTGTACAGTACACCGGACAGA
 GTGCAGAGGAGCTGAGCTTGTGAGGGGGCACTCATCCGTCTGCTGCCCGGGCCAAAGATGGAATAGATGAGC
 GCTTCTGGAGGGGAGAAITTTGGGGCGCTGTGTGGGGTCTTCCCTCCCTGCTGCTGGAAGAGCTGCTTGGCCCC
 CAGGGCCACTGAACTCTCTGACCTGAACAGATGCTGCGCTCCCTCTCTCCAGCTTCTCCCACTGTGAC
 TCACTCTGTGTGATGGGCCCTGACACTGTCTGCTGCTGGGGACAAGCCCTGGACTTCCCTGGGTCTCTGG
 ACATGATGGGCACTGCACTCAGGCCGATGCGTCCACCACTCCCGCGCGGCTTAAAGCCCGGATCTTGGCCACC
 CAGATCCCTCACCCTGAGAGGGCAGGAGCCCTTGACCCCACTGATGCTGCTGCTCCCTATCTTCAAGCTGTGACA
 CACCACTCAATGATCTCAGACCAACACAGCCAAAGCTGCAATCGCCCTTATTTCCACCTCACTCCAAAGGT
 GGAAACTTGCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTTCCATTGTTCTATCATCTCTAGGACC
 GGAACACTACTCTTCTCTTCTGTATGACCTTATCTAGGTTGGTGAATGCTGAAATCTCTGGGGCTGGAACCC
 ATCCATCAAGGTCCTAGTAGTTCTGGCCCACTCTTCCCAACCTGGCTCATGACCCACCCCACTCTGGATG
 CCAGGGTCACCTGGGGTTGGGCTGGGAGAGGAACAGGCCTTGGGAATCAGGAGCTGGAGCCAGGATGCAAGCAG
 CTGTAATGGTCTGAGCGGATTATTGACAAATGAATAAGGGCACGAAGGCCAGGGCCCTGGGCCCTTTGTG
 CTAAGAGGGCAGGGGCCCTACGTTGCTATTGCTTTAGGGGCCCAACACGGGCGAGGCGCTGCTCCAGCTGCCAC
 GCTCTATCATATGGAGCGAGGTGTTGGGGAAGCGGGGACGGCAGCTGTTGAGGCGAGGGGAAGGAAGAGAC
 TGAGGGGCTGTACCTCTCTGAGGCCCCAGCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
 AGCTGGGGGCACTGCTGTCCAGTGGAGGGGAGGGCTTTCAGCCCCACCCACCCCTGGCCCTGCAGCTGGTAG
 TCCATCAGCAATGAAGGAGACTTGGAGAAGGAAGAACTTGTGCTTCTGTTCAAGCTGTGTGCGACG
 TTTTCCGCTGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGGATTATAGAGGAGCTTAAGCCTGC
 AGTTTACTCTGGGGGTTCAGGGAGCCGAAGGCTTAATAGTTTAAAGTAGTGATGGGAAGATGAGATTAACTCTA
 TTTAGGCTGGGAGCTCACTCACTACTCTCCTGCTGCTGCTGAGAGCAACTGAGAGAAGGGGAGGGG
 TCAACAATGAGAGCAGGAGTAGTCTTATCATGTGCCCCCAAGTAGAGAGCAATAGAGCCCAAGCTCAGTGC
 AGTCCCGGCTGTGTTTTCTACTGTGATCAGAAAGTGTCTGGTTGCTTGGCTGCCAATTTGCCCTCTGTAGTGG
 CAGCCCTGGGCTTGGGCCCCCTCCCTCGGCCCTCAGTGTGGCTCTGCAAGAGCTTGGGGTTCCTTCAAGTG
 CAGGAGGGTTAGGCTGCTGTCCCTGAGTCTCTCACTCTGATGGGGGGCTGGCTAGGACATGGGGCTGTGGCC
 TCTCAGGGGACGCTCTCCATGAGAGCATCCTGCTTGGCTGGCTCCCGGACCCCTGACCAACCCCTG
 GGTCTATCTCCCCACCAAGGCCCACTCCTGCTGTGGGGAGGCCATCAGGTGTTCTGTGCACTCATAGGCT
 TCTCAATGTGTCTCACCGGAACCTGGGAGGGAGGGAACACTGGGGTTTAGGACCAACAATCAGAGGCTGCTGTG
 GCCCTCCCTCTGACCCAGGATCTCTGAGTTTGGTGGCTACTTCCCTCTGGCTAAGGTAGGGAGGCGCTCTC
 AGATTGTGGGCACTTGTGTAGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGAGGCCACTT
 TGGGATCAGGTCGCTGATCACTGGGCCCTTACCTCAGCCCCCTTCCCTGGAGCACTGCCCACTGCCCCA
 CAGAGAACAAGTGTCTTCCCTGCTCCGGGGCGGCTTTTCCCTCTTGTGAGAGCTCCCTCAGGCGTGGAG
 GCTCTTGTCTGGCTGCAATGATGCAAGGGGCTGAGAGGCCAGGTGCACTGTGATGATGGGAGGGGCTC
 CGCTCTCAGGCTGAGGTGCTTCCACACTGGACAGCAGGAGGAGGTGAGGGTAACTTTCCATTTCCCT
 TCATGTTTTTTTCTACGTCTTTCAGCATGCTCCTTAAACCCCAAGAGCCCAATTTCCCAAGCCCAATT
 TTTCTGTCTTATCTAATAACTCAATATTAG

FIGURE 178

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEPPAPQALATRALPCPAHVVFQYQAGREDELTITIEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSPSSQSDNPGCAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPELSDPEQMLPSPSPPS
FSPAPTSLVDGPPAPVLPQDKALDFPGFLDMMAPRLRPMRPPPPPAKAPDPGHPDPLT

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GAAA**TAA**CCCTCACTATCCCGGCTGCCCTTCTGGGCACCGGGGCTCGGACTTAGCTGGGAGAGAGAGACTT
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CGAGTAGCTGAGATTATAGGCACCTACCACCGCCCGGCTAATTTTGTATTTTATAGTAGAGACGGGTTTCAC
CATGTTGGCAGGCTGGTCTGCAACTCTGACCTTAGGTGATCCACTCGCTCTCATCTCCCAAGTGTGCGGGAT
ACAGGCTGAGCCCGCTGCTCGGCCACGCCCAACTAATTTTGTATTTTATAGTAGAGACGGGTTTCAACATGT
TGGCCAGGCTGCTCTGAACTCTGACCTCAGGTAATCGACCTGCTCGGCTCCCAAGTGTGGGATACAGG
TGTGAGCCACCGCCGATACATATTTTAAATTGAATTCTACTATTTATGTGATCCTTTGGAGTCAGACAG

FIGURE 179B

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FIGURE 180

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><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
FPEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLQGAPELLGGAEP
GTYLTGTINGDPESVASLHWDGGALLGLVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPNCNVKAPLGSPPRPRAKRFAASLSRFVETLVVADDKMAAFHGAGLKRYYLLTVMAA
AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRGNTPEDSGPDHF
DTAILFTRQDLGCVSTCDTLGMADVGTVCDFPARSCAIVEDDGLQSAFTAHELGHVFNMLHD
NSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNI PQAGGWGPWGPWGDCSRCTCGGGVQFSSRDCTRFPVPRNGGKY
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVA PQDQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVQVQGRCIHAGCDRIIGSKKKFKDKMVC GG DG
SGCSKQSGSFRKFRYGYNNVVITIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSEFFVPRPT
PSTPRPTQDWLHRAQILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTTCTAAATGCAGAAGCTTTTAAATCC
 AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCT
 AATTGTCTCTGTTTTGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTG
 ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTTGGAAGTGCACGACTT
 TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGA
 TTAAAGTGATTCTGAATTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTTCTTTGAACAGTCAGTGATTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTTCTTAAAAATTCCAAAATTTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAAGT
 AGAGAAGACCGTCA CGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG
 AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCGCTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGTGTCATCATGCCTTGTAACGGTGGGTGGCCC
 GCATGCTGGGGAGGGTCT**TAA**TAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
 CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAAAA

FIGURE 182

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTILIVLFWGSKHFWPEVPPKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIVFVGLQKCFIKT
QIKVIPFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNKILEICDNTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLDERGYCCICYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWW
ARMLGRV
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Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAAGTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCGCACCA**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCTTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCTTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAAGTGCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCGCGCCCTCATGGTCATCTCCTGCCCTGCTCTCGGGCATAGCCT
 GCGCCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
 ACCTTTGCCATCCTCGGCGGCACCTCTTCATCCTGGCCGGCTCCTGTGCATGGTGGCCGT
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCTTGCTTTGCCTGTCTGCCAGGACGAGGCACCTTACAGGCCCTACCAGGCCCCGCC
 CAGGGCCACCACGACCACTGCAAAACACGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
 AATGGAGGCAGGGGTTCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
 ATGTGAATGCCAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTGTATTTATTATATATAT
 TTATGTGGGTGATTTGATAACAAGTTTAAATATAAAGTACTTGGGAGTTTGGTCAGTGGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLLITTLILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLIGGTLLCLSCQ
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:**Signal peptide:**

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

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FIGURE 185

GAGCTCCCCTCAGGAGCGGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGGCAGGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCTCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC
 CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
 GTCTGTGTTTGGCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTTCAGACCAGGTACACATTTGGTGGCGCTCTGTTCTGTG
 GGCTGGGTGCTGGAGGCCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
 CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTG
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAAACAAGAAG
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
 TGTGTAAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCGGAGAGCTCACCAAAA
 AACAAGGAGATCCCCTCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
 TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC
 ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA
 TTTCCAGCTTATCCCCAAGAAAACCTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT
 CTGCTGTTTGAATTTGTCTCCCCACCCCACTTGCGTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACTG
 TGATCTTAAAGTTACCAACCAAGTCAATTTTCAGTTTGAGGCAACCAACCTTTCTACTG
 CTGTTGACATCTTCTTATTACGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
 TCCTCTTTCTGTGCGGGGTGAGAAATTTGTCCTAGATGAATGAGAAAATATTTTTTTTTAAT
 TTAAGTCCTAAATATAGTTAAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTGTCT
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATCCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCGAGAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTTACAAAATACAGAGAGAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG
 AGGTTGGGGCTGCAGTGAGCCATGATCACCACTGCACTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA
 ACTAATTCTTTAA

FIGURE 186

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGG
 GAGTCCAGCTGGCTAAAACATCATCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTTGGTGGTGGTGAATGGTGGGCACAGTGGCTGTCACTGTGCCTCAGTGG
 AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTTTTGAAAACCTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTGCTGG
 CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
 TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA
 GGTGAAGGCTCACATCTGTCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
 TCATCCTCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCAAAAACGTGAGCTTGGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACCTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCAACCG
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTTAACTTTACTATAAAGC
 CATGCAAATGACAAAAATCTATATTACTTTCTCAAATGGACCCAAAGAACTTTGATTTA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA
 GCTATTTTCAGCAGAATGAGATATTAACCCAATGCTTTGATTGTTCTAGAAAAGTATAGTAAT
 TTGTTTTCTAAGGTGGTTCAGCATCTACTCTTTTTATCATTACTTCAAATGACATTGCT
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACATTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAAGTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTATAATGA
 AGATTAAGTGAAGGCTTTAATCAGCATTGTAAAGGAAATGAATGGCTTCTGATATGCTG
 TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTT
 TTCTGTGTATTAATTAACATTTTTTAAACGCAGATATTTGTCAAGGGGCTTGCATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAAATATTTTTGTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAGAGCAGAAAAATATGTCTGGTTTTTCATTGCTTACCAAAAAACAAACA
 ACAAAAAAGTTGTCTTTGAGAACTTACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG
 TCATTTTTGTCTGTGAAAAATAAATTTCTTCTGTGTACCATTTCTGTTTGTGTTTACTTAA
 ATCTGTAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAACTGACAATCCAATTTGA
 AAGTTTGTGTGACGCTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTATA
 TTAATAAATTTGACATTTTTTCTAATT

FIGURE 188

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCCATGGCCTCTGCCGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
 CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTCGCTGGTGCAAGACACCGGCC
 AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGTGCCACAGGACCTGCAGGCTGCACGT
 GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTGCGCTTGCTGCTCTACCTTGCTGGGGC
 CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA
 TTGTCTTTGTCTATCTCAGGGGTCTTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
 ATCCGGGACTTCTATAACCCCTTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT
 CTACTTGGGTGGGCGGCCTCAGGCCTTTGTGTGCTGGGTGGGGGTGCTGTGCTGCACTT
 GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCGCTACTCAACATCTGCCCTT
 GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTGACGTGGAGGGGAATG
 GGGGTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGT
 CGTACCTTTTGTCTTCTGCCCTCCTGCTATTTTCTTTTACTGAGGATATTTAAATTCATTT
 GAAAACAGGCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCTTGG
 ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
 CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
 TGTCCCAAGAGTTCTGCTGCTGCTGGGGGCTGGGCTTCCTAGATGTCACTGGACAGCTG
 CCCCCATCTACTCAGGTCTCTGGAGCTCCTCTCTCACCCTGGAAAAACAAATCATCTG
 TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCTCCGCTCTGATAAGACG
 TCCACCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
 CTTCTGCCCTGCCCCCTCGTCTCACCCCTTTACTCACATTTTATCAAATAAAGCATG
 TTTTGTAGTGCA

FIGURE 190

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGWLMSCVVQSTGQM
QCKVYDSLALLPQDLQAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLGGGLLCCTCP
SGGSQGPPSHYMARYSTSAPAIRSGPSEYPTKNYV

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
 AGCATCTTCTACCACCTCGAATTGAACAGTCTTCAAAGTAAAGGCAATGGCATTTTATCCC
 TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCCTGGCATGGTGGGACTCTTGCCACAACCTC
 TCTGCCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
 TGGGAAGGGCTCTGGATGAAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGCTCCTTGTGGCTCTCCCGCTGCCCTGGAACAGCCCGGGCCCTCATGTGTGTGGCTG
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
 GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCCTCTTCATCCTGAC
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
 ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
 AGCGCTGCTGTCTCTTCATTGGAGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT
 ATGGACTATGGTCAATGTTTTTTATAAAGTCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
 GAACCTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
 GACCCAAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
 TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAAG
 GTTGAAATTGATATTCTATAACAATAAACATATACCTATTCTA

FIGURE 192

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737

><subunit 1 of 1, 173 aa, 1 stop

><MW: 18938, pI: 9.99, NX(S/T): 1

MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV

Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCTGCCCCATCA
CATACCTACCAGTTTGTGGTCTGACTACATCACCTATGGGAATGAATGTCACCTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCAGGCTCTGACTG
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCCATGGCTGCCTCCCCCGCGGCCCTGCTGTCTTGCCCTGACCGGGCTGGCGCTGC
TCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACTTAACCATGACTTGCACACGCTGTACAAGAAGCAAATAGCGATTCT
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTGCTCTATTTACAGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAGAAGAGTTAAACAACACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLCWGPGGISGNKLLMLQKREAPVPTKTQVAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDDYYQRHYD
EDSAIGPRSPYGFRRHGASVNYDDY

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCCCCGGAAGTGCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC
GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
CGTCCTTTTCTCGGTGCTTGCCCTGCCCTTCTGGTGCTGGCCCTTGCCCTGGGTCTCAACGCACA
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTAGGGACCCCAACGCCATCCCAGCCCAGC
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTCACAGCAACACCGCCAG
CCCCGACTCCCCGCAGGAGCCCCCTCGTGCTACGGCTGAAATTCCTCAATGATTGAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAGGACCCAGTTTCCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGCCACGAGAGTCGGTCCC
CCAAATCCCCCTGCCCGCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAATCGGCAGCCT
GCTGCTGCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTACCCTGCTCCTCAGTCTCCTG
GCCTTTGCCATGTACCGCCCGTAGTGCCTCCGCGGGCGCTTGGCAGCGTCGCGGCCCCCTCC
GGACCTTGCTCCCCGCGCGCGGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG
CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCGCCGAGAGGACTCCCGGGAAGTGGCGGAGG
CCCCGCCCTGCGACCGCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
CTGGGAGTGGGCTCCTCGGGGTCGGGCATCTGCTGTGCTGCTGCTCGGCCCGGGCAGAGCCG
GGCCGCCCCGGGGCCCGTCTTAGTGTCTGCCGAGGACCCAGCCGCTCCAATCCCTGAC
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTGCGTGGGAGGCTGGTGAAGGGGAGCGGGGAG
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTAAAAAAAAA
AAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRCLKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPCCPPGS
EPGPSGLEIGSILLPLLLLLLLLLLWYCQIQYRFFFLPTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

FIGURE 199

GAGATTGGAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
 ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
 TCAGCTGCACCTCCTCCCTCCAAGGATGACAAAGCGCTACTCATCTATTTGGTCAGCAGC
 TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
 GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG
 AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC
 TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA
 CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGAGGCATCCACTGCGCAAAAAGGA
 TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGTTGCACTGTTCAGGCCGG
 CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATTGAAACAGGGTGCGGGTGCAACCGTGG
 AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA
 CTTTCATGTTATTTTCTTCCCTTCCATTTACAACATAAACTGACCAGAGCCCAGGAATAAA
 TGGTTTTCTTGCTTCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTAT
 TTGTAAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCNVDCQDLLNPNLLAGIHC AKRIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTATTATACAAAGGGGGAAAGAAACACCTGAG
 CAGAATGGAATCATTATTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGGAGGGAAGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAG
 TTGGGGTGAACTTTGGGTCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCTTGACACAGC
 TGTGTGGCAAAATGTGAGGACAGGTTAAGTGACTGGCAGAAAAACTTCCAGGTGGAACAAGCA
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAAGCTTGACATGAC
 CTGTTGCATTTTGGCAAGTTCTAGCAAC**ATG**CTCCTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCCCTCTGCTGCTCCTGATGCTGGGATGCGTCTCTGATGATGGTGGCGATGT
 TGCACCCCTCCCCACCACACCTGACACGACTGTCACAGCCCAAGCCAGCAGCACAGCCCT
 GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCCCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAGGAACCAAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTCAAGCTGGACCCAC
 GTGGCTTCCAGGAGGCCTCAGTGCCCGCATCCCTTCCAGAGGGCTGCTGCCCGAGGTGGG
 CACCCACTGTGCTGTCAGCAGCACCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG
 TTTCCATGATGAGGCTGGTCCACTCTCCTGCGGACTGTACACAGATCCTCGACACAGTGC
 CCAGGCCCTTCTGAAGGAGATCATCCTCGTGACGACCTCAGCCAGCAAGGACAATCAAG
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACAGAGCCACCGGGGATGTGCTCGTCT
 TCATGGATGCCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCAGTA
 TTACCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCTGAGAAC
 CTTTGGCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCCCGAGAGGTTGGTGGCCATGGACAGACATTACTTCCAAACACTGGAGCGTATGACTC
 TCTTATGTGCTGCGAGGTGGTGAACCTCGAAGTGTCTTTCAAGGCCCTGGCTCTGTGGTG
 GCTCTGTTGAATCCTTCCCTGCTCTCGGGTAGGACACATCTACAAAAATCAGGATCCCAT
 TCCCCCTCGACCAGGAGGCCACCTGAGGAACAGGGTTCGCTATTGCTGAGACCTGGCTGGG
 GTCAATTCAAAGAAACCTTCTACAAGCATAGCCAGAGGCCCTTCTCCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTTGACAGTGCAAAGGAGACTGGGTGTGCGACATTCCACTGG
 TTTCTGGCTAATGTCTACCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAG
 GATAAATGCTGGGATGAACGATGAATGTCAATGTGAGAAGGAAAGAGAAATTTTGGCCATC
 AAAATCCAGCTCCAAGTGACGTAAGAGCTTATATATTTTCAATGAAGCTGATCCTTTTGTGT
 GTGTGCTCCTGTGTGTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTTCATTGACTGCTGGCTGCTTA

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEAR YRLDFG
ESQDWVLEAEDEGE EYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRDWGADEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVSP
VIDVIDWKTQYQYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSFVVPGEVVAMD
RH YFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQNDSHSPLDQEATL
RNRVRIAETWLG SFKETFYKHSPEAFSLSKAEKPDCEMERLQLQRR LGCRTFWHFLANVPYEL
YPSEPRPSFSGKLHNTGLGLCADCQAE GDILGCPMV LAPCSDSRQQYLQHTSRKEIHF GSP
QHLCFAVRQEQVILQNCTEEGLAIHQHWFQENGMIVHILSGKCM EAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACACAGCTGAGGAAGACCTCAGAC**ATGGA**
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC
 TGCCCCCTCCACCGCCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACCAGCCCCAGCC
 CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCCCACGTCACTGTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATACGTGCGGAAGTCTGCGCTGGCACTG
 CACCCCAAGCACCCTCAGGCTTTGAGGAGGGGCGGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGTCCACCCTGTCTCGAGAGGATGGAGGGACCCCAACTCTGCCAATCCCGG
 ATTTCTGGACTATGGTTTTGCAGCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCCTGCGGCCATTC
 CTGTTTCGGGGGCCGTGGGGAAGGTGTGGACCCCAAGCTCTATGTCACAATTACCATCTCCAT
 CATCATTTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
 GACGCAGACCCCTAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGCCTTCGGGGACTCACCTACCCCCACCCC
 TGACCATGAGGAGCCCCGAGGGGGACCCCGGCCCTGGGATGCCCCACCCCAAGGGGCTCCAG
 CCTTCCAGTTGAACCGGT**GGA**GGGCAGGGGCAATGGGATGGGAGGGCAAGAGGGGAAGGCAC
 TTAGGTTCTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGCGCTGGC
 CTCCACAGCCCTTGCCCTCCCAAGGGGGCTGGACAGCTCCTCTCTGGGAGGCACCCCTC
 CTCTCTCCAGTCTCTCAGGATCTGTGCTCATTCTCTGCTGCCCATAACTCCAACCTTGCCC
 TCTTTGGTTTTTTCTCATGCCACCTTGCTAAGACAACCTTGCCCTCTTAACTTTGATTCCC
 CCTCTTTGTCTTGAACCTCCCTTCTATTCTGGCCTACCCCTTGTTTCTCTGACTGTGCCCTT
 TCCCTCTCTCTCAGGATCCCCTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGACGCC
 AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGA
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGACACACCACCGGAACACTCCCCAGCC
 CCACGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG
 GGTCCCCTGTCCCCACCCCTGTGCACTCATATGAAGCCTTGACACTCACCTCCACCTTTCAC
 AGGCCATTGTGCACAGCTCCTGCACCCCTCCTCCCGTCCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCTCGTCTCAATTGCACTTCTCCTTCCCACTTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTTCCTGCACACTTTACCTCTCATGTGCGTTTTCCGGCCTGATGTTGTGGTGG
 TGTGCGCGCTGCTCACTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAGCCCCCTGC
 GTGCTGCTCCAGAGTGGGTGGGAGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTCAATGG
 TCTCGTCCCATCCACACCATTGTTTCTCTGCTCCCCATCCTACTCCAAGGATGCCGGCA
 TCACCTTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA
 CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTTGGGGAGTCGCCTGCTGCATACATAGAA
 AGGGACTCCCATTTGCCCTTCCCTTTCTCCTACAGTCCCTTTTGTCTTGCTGTCTCTGGCTG
 TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCTCTCCCTTCCAGCCCT
 CCCTTTTGGGCCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGAGTCAGCTGGTTCAAGGCC
 ATCGGGAGCTCTGCCTCCAAGTCTACCCTTCCCTTCCCGGACTCCCTCCTGTCCCTCCTTTT
 CCTCCCTCCTTCCCTCCACTCTCCTTCTCTTTTCTCTCCTTCCCTTCCCTTCCCTCCTCAGGTT
 CTTCCTCCTTCTCACTGGTTTTTCCACCTTCTCCTTCCCTTCCCTTCCCTTCCCTCCTAGGCT
 GTGATATATATTTTTGTATTATCTTTTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTG
 GGATGTAAGTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAGV
PGRDGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTAAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCGCTGCCCTCACTCCCGGCCAGG**ATG**
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGAGCCCGTGGACACCGGTCCCC
CAGCCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGGCCCGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA
GGGGCCGCGCCCGCGCGCGCGCGACTCGGCAAAAAAAAAAAAAA

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FIGURE 206

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVVESTSPGREPVDTG
PPAPTVA GPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCCGTTGGTTGGTGCGGGCTGAAGGGTGTGGCGCAGCAGCGTCGTTGGTTGGCCGGCGG
 CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGGCGCTGGCCCA
 CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
 ACTTCAAGTCCTGGTGGGTGGGCAGCATCCCCGTGTGAGGGGCGCTGCTCACCAGCTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
 CCGGGTATTTCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCCTAAGTAGCCC
 CCAGAGGCGCTGGGAGTGTGGCACCGCCCTCCCCTGAAGTTTGCTCCATCTCAGCTGGGG
 GTCAACCTGGGGACCCCTTCCCTCCGGGCATGGACACACATACATGAAACCCAGGCCGCAT
 CGACTGTGACGACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACGCACAG
 ACTCGCACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
 GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCTTCCAC
 CTGGCTGTGATCGGGTAGGGCGGGGCGGTGGGTTGAGGGGCGCACCACTTCCAAGCCTGTGT
 CCCACAGGTCTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACACATAAATAAC
 TGGCACAAAGTAAGTCCCTCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
 GGTGAGTATGTGTGGGACACAGGCTGGCTCCCTCAGCTCCCACGTCCTAGAGGGGCTCCCGA
 GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCTTTTCTCCCTCAAAG
 GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTCTTAAGGGTCCCCATAGGGTCTGGTTCC
 ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC
 ATGGAGGGGCTGACTGCCCCACATTGCCTTTGAGACAGGACACGAGCATGAGGTAAGGCCGC
 CCTGACCTGGACTTCAGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT
 AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC
 CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
 CCTGGGACACACAGAGCCACCCCGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
 AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC
 ACGAGGGTGTCTGGATGTGGCCACACATAGGACCACACGTCACGCTGGGAGGAGAGGCCT
 GGGGCCCCCAGGGAGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
 CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
 TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC
 GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC
 CTCAGGACCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
 GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGACAGAGCTGCGGGA
 TGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAITIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGACAATGGAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTG
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCTAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA
 TAGCATGGTGCAAAAATCCCAGGCGTGTCATTTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCCGCTGGTAGACAATGAACAACG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGGTACAACCCGTGACTGTGATTGGGTTATTC AACAGCG
 TAATTCAGATTCATCTCCTCTGATAATGAACAAGGCCTCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAACATAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAAACTTTTGTGATGGATTCCCTAAGTGGAATAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTTGACTTCTCCTTGGAACCTACATATGGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCCTGCCAACACACACACACGCGTGCACACGCGCAGCGTGCACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC
 TTCTTCTTCTTTTAAATTTCAATCTCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTGCTCTTTTAAGGTTACCTAAGGGT
 TGAACCTCTACCTTCTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG
 ATGGTTTTTAACACCTTTGTGAAATTGTCTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACCTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCCC
 TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA

FIGURE 210

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVFILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDWDLTLPATAEVSVQHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCCGCGCTGGGACCGGAGTGGGGAGCGCGCGTGGAGGTGCCACCCGGCGCGGGTG
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
 GACGCGGCGGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGACGCTCCGCGGAGCCGGG
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGGTGGCGGCGGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTTGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCCTGGAGCTTCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTC
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
 TGTCTGTAGAAAAAGAAATTTGCCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
 CTGTGGTCTTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTACCAGTTAAGCAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
 AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAAC
 AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATC
 CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT
 AGCCTTGGAGACCCAGGCAAGGACAGTACAGTGTACTCACAGAGGGAGAGAAAGATGTGT
 ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTCATGA
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTGTCTGTTTTTGTACTTTCTTTTC
 AGGTCATTTACAATTGGGAGATTTCAGAAACATTCCTTTACCACATCATTTAGAAATGGTTTG
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTGAAGTTTTTCTCACT
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGACCCCTTG
 AAATGTGTCATATCAATTTCTGGATTATAATAGCAAGATTAGCAAAGGATAAATGCCGAAG
 GTCACCTTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTTGCTT
 GAGAACTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKASINNIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTYGCSTSESLSPVKQAPRKSPDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGT CAGCAGTGACTGCCCGGGCTGCCGCC
 CCCGGGGGCTTGGCCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGCGGGGCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGCCCGGCGCAGTCCCCCGCGGCCCCGACCCCTGAGGCG
 TCGCCTCTGGCCGAGCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCGGC
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAAACTGGATCTTGATATTCAGTACAACATTATGTTCCCGAATCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGAATTCTG
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
 TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT
 ACTAAATTTAAACAGAGCAGGAGAATGAAGCCAAATGCCGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAATTC AATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
 ACTTTTGGCTATACCCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAATATTTGGA
 CTATATGCAGAAAATATTCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGTCTGTTTCTCATCTGTAAAGTGAAGGAAGTAAAAACA
 TGTTTATAAAGTAAAAAAA

FIGURE 214

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGAATTCGGCTCG
 AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCCAGTCGAGCCCGGGGACGCGGCTGCCGGGCCGGGACT
 GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCGTGTGGCACGGTGGGGCTGCT
 GCTGGAGCACTCATTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGCGACCCGG
 GGCCCTGGATGGCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTTCGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCTGTTCCTCATGATGTACAGG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
 TTGCTGTGTGCCACCCTCCCTGTAAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTGTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTTCAGAAACCCAG
 GAATGGCTGTCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTGTGTGGCAGTTTAT
 TAAACTGTCCCCAGATCGACACGCAAAAAAAA

FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
 DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPRRPGALDGLEA
 GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
 LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWYIIPVVLFLMMSGAPDTGGQ
 GGGGGGGGGGSGLCCVPPSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

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FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGAGCCGAGCCACAGCGGGGAGGGTGGCCCTGGCGGCCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCGCAGACCGGGGCAGCAGGTGCTCCGGGGGCCACC
ATGTGGTGACTGCCTACCTTGCTTTGTAGCCCTCCTGGCCCTCCTGCCTGGGGCTGGAAC
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCGTTTC
 AACTGGACTTCTATCAGGTCTACTTCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTACTACTTCTGGAAGGTCAAATGCCATCCTCTATGTCTG
 TGGCCTTGCCCTCTACAGTCCCTTTTGGCCTAGTGGCCCTCCTCCCTTGTGGATTGGCTGGGTC
 GCAAGAATTCTTGTGCTCTTCTCCCTGACTTACTCATTATGCTGCTTAACCAAACCTCTCT
 CAAGACTACTTTTGTGCTGCTAGTGGGGCAGCACCTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCTGCTGAGT
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCCCTTGGCCCTTCGAAACTGGGGGAGAACTATGACC
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCCTGCTCCTGCTCGGACCGCCGC
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTCATCTTCATCTTTGTCTTCTCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCAC¹TACTGGCTTGCCTAGGGCT
 CCTTGCTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTCAGCATTTGCTCTG
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCCTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTTACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATTCAGCTATCCGGGATTGTACAGATCTCTCTGT
 GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTGGGAGGACATGA
 TGGGGGTGATGGACTGGAAGAAGGTGCCAAAAGTTCCTCTGTGTACTCCCATTTAGAAA
 ATAAACACTTTTAAATGATCAAAAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
 LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
 QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
 VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQAFSRTCAGGLRCLLSDRR
 VLLLTGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ
 PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET
 EQAGVLNWFVRVPLHSLACLGLLVLHDSDRKTGTRNMFSCSAVMVMALLAVVGLFTVVRHDA
 ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
 314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGCGGGGCGGCGAGAGGAAACGCGCGCCGGGCGGGCCCGGCCCTGGAGATG
 GTCCCCGGCGCCGCGGGGCTGGTGTTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCTCCGCTGAACCTCCAGAGGCCCTGCGGGGAAGTCTGAGCAACGGTTTCTTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
 CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
 TGGTAGAAAGAGTTTGTCACCATTCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCAGG
 GCCCCAAGGGTGTCTCATGCTACAGAAGAGGCAAGAGACAGGCCCGAGGGCTTCTGGCTA
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACT
 CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
 AGTGGTTTAAAGAGCTGGTGGTTTGGGGACTCAATAAACCTCACTGACTTTTGTAGCAATAAA
 GCTTCTCATCAGGGTTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

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FIGURE 221

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 AGGCCAACCCAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTGCTATGACCACC
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FIGURE 222

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPHYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNKSSIHCMDLSQRYCLMAVFNVITYLENEDSE
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Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCCTTCTGGATGGGGGCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG
 GGTGCCCCGGCACACCAGACGCCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG
 CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGAAGATGTAT
 GGCCCTGGAGGAGGCAAGTATTTAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT
 GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG
 ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
 ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA
 GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAG
 AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTTGGC
 TTTGAATGGAATTATCCACTAGAGGAGCCGACCACCTGAGCCACCAGTTAATCTCACATACTC
 AGCAAACCTACCCGTGGGTCGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
 GTGGTGGTGGCTGATGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
 AATAAAGCTTCTGCAGAAAA

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FIGURE 224

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FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAAC TGGGTGCTCATCAGCGGAAC TCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAAT TGGCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATGTAGGATCCAGTT
 TTTTTTTTAAACGCCCCCTCCCAACCCCCCAAAAACTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
 TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCCAAGGGGTCCAATTTTTCTTCTTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGGCTGTCATGCAACTGGCCCCTAAGCCAAGCAAAGACCTAAGGACGACCTTTGAA
 CAATACAAAGGATG GGGTTCAATGTAAATAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTTGTCCTTCGCTATAACAGCCTTCAAAAACCTAAGTATAAT
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
 TCTCTATTTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACTTGGATCTGTCC
 TATAATCAGCTGCATCTCTGCGGATCTGAACAGTTTCGGGGCTTGCAGGAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATCCAAGACTGCCGCAACC
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTGTCTGGC
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACAAATCAATTTTCCAAGCTCAACCTGGCCCC
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTGTGAGTGAATAAAATCAGTGTCTATAG
 GACAGACCATGTCTTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC
 GAAGCTTTTCAAGTGGACCCAGTGTTTTCCAGTGTGTCCGAATCTGCAGCGCCTCAACCTGGA
 TTCCAACAAGCTCACATTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
 TCAGTCTTGTCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTG
 AAAAGTTTTAAAGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT
 TTGATCTGCCCAGGGCTCTCCAAAGCCGACGTTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT
 GAGAGCAAAACCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG
 TGCTCGTCATCCTGCTGGTTATCTACGTGTCTATGGAAGCGGTACCTGCGAGCATGAAGCAG
 CTGCGAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAT
 GACTCCAGCACCAGGAATTTTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA
 TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAGAGCTCTTAAAGCTGGGAATAAGTGGTGCTTTATTGAACTC
 TGGTGACTATCAAGGGAACGCATGCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG
 CAAGATCCTTCTTGTCCGTTTTAGTGCAATCATAATACTGGTCATTTTCTCTCATACATA
 ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAACCTCCGTTTAAATAAA
 TACCTATTGTATAAGACCTTTACTGATTCCATTAATGTGCATTGTGTTTTAAGATAAACT
 TCTTTCATAGGTAAAAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTPLLTLMLSSAERGCPKGCRCCEGMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKEHLHLEHNQFSKLNLALEFPRLVSLQONLYLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNSNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPPLPPTVGATEPGPETDADAHEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACTACTATCCTAAGTTGACTGTCCTT
 TAAATATGTCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
 TGTTCGCCGTATTCCAGTTGGTGCTCTCGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGTGGCTGAGGAGACCCCGA
 ATTGATTCTCACAGGCGACCATGGCAGTTTTTGTGTTGGAGACTTGGACTCTATTATATG
 GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCTCTGCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
 AAAACAACCTGTATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATCCA
 AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
 GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAATTTTGGTCATGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGTACAC
 AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
 CTAGCATGGGGTCCATAAAAAATTATTATAATTTAACAATAGCCCAGCCGAGAATCCAACAT
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
 CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG
 GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
 CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
 AAACATCAATAGATATCTAAAAA

FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCCEEDCMVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPFPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGAGCCCCGCTTATTA
 GCTCTCGCTGCGTCGCCCGGCTCAGAAGCTCCGTGGCGGGCGGCACCGTGACGAGAAGCCC
 ACGGCGAGCTCAGTTCTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT
 CCTCTTCAAACCTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGC
 TTACCTCAAGTTACCATTTTTCAGTCAAGTCTGTTTGTCTCTTCAGAAATGCTTTTTTA
 CAATCTCAAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATT
 TGGGGATTGATGTTACTGCACATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAACTACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAAAGA
 ACACAGTGGATGTGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAAAT
 GCTGTCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAGTTGACTATAT
 TGTTGTGAATGGCTCAGCAGCCAAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
 CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
 AGAGCAATACCTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCAATGGAAC
 TCTAATCTGTACATAAAAAATTTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATG
 CTGTACTATGTCCTTTAAAGAGAATTTGGTAACCTGGTTGATGTGGAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATTCT
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGATGTTTAA
 TCATTCTGTCATTTTGTCTCAATAGATGTAACCTGTAGACTACGGCTATTTGAAAAATGTG
 CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAAATGTATTGATTGCACTATCCTTCAGAATAACTGA
 AGGTTAATTATGTATATTTTTAAAAATTAACCTTATAAGAGTATAATCTTGAAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAATAGTT
 GTAACTCTAATCTTACTTATTGAAGAATAAAAGATATTTTTATGATGAGAGTAACAATA
 AAGTATTCATGATTTTTACATACATGAATGTTCAATTTAAAGTTAATCCTTTGAGTGTCT
 ATGCTATCAGGAAAGCACATATTTCCATATTTGGGTTAATTTGCTTTTATTATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAA
 GGTACTTTTGTGCTGCATTAATTTGCTTGAAAGTGTTAACATTTATATATATAAGAGTATC
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
 TTAATAAAGAACATTTAAATATAAATATGAAGATTGACTATCTTTTCAGGAAAAAGCT
 GTATATAGCAGGGAACCTAATCTTGGGTAATCTAGTATAAAACAAATATACTTTTAT
 TTAATTTCCCTTGTAGCAATCTAATTGCCACATGGTGCCCTATATTTCTAGTATTTTAT
 CTTATAGTAACCTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT
 TGTATTGTTCTGCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATAAAA
 TAAATATGTGAATATTTGTTTCATGAAAGACAGATTTCCAATCTCTCTTCTCTCTCTGTA
 CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

FIGURE 230

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
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Important features of the protein:**Signal peptide:**

amino acids 1-26

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FIGURE 231

CGCGGCCGGGCCGGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCGTGGCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAACCCGGCCATGCT
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG
 GTGGATTGTAGCGGCTGGGCCCCACATCATGCGGTGCCATCCCTCTGGACACAGCCCA
 CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCCGGCT
 ACACAGCGTGTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCACCTGCCC
 TTCTCCCGCCTTCGCTACTTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
 AGCCGAGAGCTTCACCAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACCCAGCTCCGGG
 AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCCGGCACTACACGTGGACCTCTCC
 CACAACCTCATTACCGCCTCGTGGCCACCCACGAGGCGCGGCTGCTTGGCGCCACCAT
 TCAGAGCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC
 TGCCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCTATTGGTCCGGGTGCCTTCGCGGGG
 CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTTCCGTGAGCTACCGGCGCTGCAGGTCTTGACCTGTGCGGCAACCCCAAGCTTAAGT
 GGGCAGGAGCTGAGGTGTTTTAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC
 AACCTGGTGGCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT
 GGGCCAGGATGTGCGGTGCGGCGCCTGGTGCAGGAGGGCACCTACCCCGGAGGCTGGCT
 CCAGCCCGAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCACCC
 ATCTTG**TGA**CAAAATGGTGTGGCCAGGGCCACATAACAGAGCTGTCTGCTGGCTGCCTCAG
 GTCCCGAGTAACCTATGTTCATGTGCCAACACCAAGTGGGGAGCCCGCAGGCCTATGTGGCA
 GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
 AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCAACCATGAGCAGAGGGACTTCGATGCCA
 AACAGACTCGGGTCCCTCCTGCTTCCCTTCCCACTTATCCCCAAGTGCCTTCCCTCAT
 GCCTGGGCGGCTGACCCGCAATGGGCAGAGGTTGGGTGGGACCCCTGCTGCAGGGCAGA
 GTTCAGGTCCACTGGGCTGAGTGTCCCTTTGGGCCATGGCCAGTCACTCAGGGGCGAGTT
 TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCGCTTCATCCTTTCTAT
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAGAATCAAGTCCACCCTTCTCATGTGAC
 AGATGGGAAATCAGGCCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCTTGGGGCAGTGGC
 ATGACTGGAGCAGCAGCCTCCTGCCTCCCAAGCCCGGACCCAATGCACCTTCTGTCTCCTCTA
 ATAAGCCCAACCTCCCGGCTGGGCTCCCTTGCTGCCCTTGCCCTGTTCCCCATTAGCACA
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTTGGGCCCTTGACCAAGCT
 GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT
 CCAGCCTAGCCAGTTTCTCACCTTGGGTGGGCTCCCGAGCATCCAGACTGGAAACCTACC
 CATTTTCCCTGAGCATCCTCTAGATGCTGCCCCAAGGAGTTGCTGCGAGTTCTGGAGCCTCA
 TCTGGCTGGGATCTCCAAGGGGCTCCTGGATTCAAGTCCCACTGGCCCTGAGCAGCAGCAGC
 CCTTCTTACCCTCCAGGAATGCCGTGAAAGGAGACAAGGTGCTGCTGCTTGTCACTTTGTAAT
 ATTGTCTTGGGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGCTTCCCCACCTGCCTAGC
 CCATCATCTATCTAACCGGTCCCTTGATTAAATAAACACTATAAAGGTTTAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGLTHLSLASLQRLPELAPS
GFRELPGIQLVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV
QDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCAGTTCCCCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA
 AAACAAGTTTGTGACATTTCCCTGAAATGTCATTCTCTATCTATTCAGTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC
 GGGAGGCTTGGCAGTTTTTCTTACTCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCC
 TCTAGTCTTGCCCTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCTATT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGAT
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAAATATCTT
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGTCTATTTAATGTATTT
 ATTTTTTTACTTGGACATGAAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
 AGCAGGTGATGTATTTTTATACAGTAAAAAAGGACCTTGTAAATCTAGAAGAGTGGCT
 AGGGGGGTATTCAATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTGTGATGTGAATT
 GCACATCTACCTACAATTACTGACCATCCCAGTAGACTCCCAGTCCCATAATTGTGTAT
 CTCCAGCCAGGAATCTACAGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261.aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGGLTCWALTAEPGWGQNGGATTTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSLFTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAQAVVKALG
ELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
 CGAGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
 TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCCTTGGAATCAGTCATTGGAGGGATGATG
 GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACCTGACCTAGTGAAGGTTCAGATGCAAAAT
 GGAAGGAAAAAGGAAACTGGAAGGAAAACCATTCGATTTCGTGGGTGTACATCATGCAATTTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCAATATACAA
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAAACACTACTTGGT
 ATTGAATACACCCTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
 TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTCAAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACCATCTTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTTTAA

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEH
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTFWSMVFWLT
YEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
TTAAGAAGTAAAAATGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGAGGTATATTGTTTTTTACAGGC
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
TTCATTGGTTTCATGTTGATGTTTGGGTCACCTATTGCTCCATGTGGATTCTTTTTGGTGC
ATATGTTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACTTA
TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCAGAGCTATGGACCTGAGATCAC
TTCCTTAAGTCACATTTTCTTTTGTATATCTGTTTGTAGATAGGTTTTTTATCTCTCAGT
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTT
TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTCATTGCATAGACTGTTAATATGTA
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAA
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG
CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT
AAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC
TGAGGCAGGAGAATCGCTTGAACCCGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
TGCACTCTAGCCTGGGGGAGAAAGTGAACCTCCCTCTCAAAAAAAGACCACTCTCAGTATC
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
TAAAAGGTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA
AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGGCCCGCAACACTCCGTCTCACCCCTCTGGGCCACTGCATCTAGAGGAGGGCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCAGGGTGGT
 GGTGAGCTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAAGCTGACCCCAAGCCACCCCTTACCTGGACAG
GATGAGAGTGTCAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTTTATTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGTGGCTGGCA
 GCCTCGCCACCAAGGAGATCCAGGTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACACTACTTTGCGTTTAAAAATCTGCAGTGGGGCCGCCAACGTCTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCCTAAACATC
 GCCTTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTTATGCACCTAGTGAAATTCTTAAAGAAATTCGGGGGGTGCAGTGGTGTGGTGG
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTG
 GGGAGTTCTTACGCAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAAGCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGC
 TGTGGCTCTTCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGTGAGGAGGAGGAGCAGGGGTGCTGCGTGAAGGTGCTGCAGGTCTTGCACGC
 TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCCTCCACAGCACATCCTACCCGAAGACC
 AGCCTCAGAGGGTCTTCTGGAACCAAGTGTCTGTGGAGAGAATGGGGTGTCTTCGTGAGGG
 ACTGCTGACGGCTGGTCTGAGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTA
 TTTTGTGCTGGTTTTGAAAAAAAAAAAAAAAAAAAA

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYSMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCTCTGGGGAT
 CCAGAAACCCATGATACCTACTGAACACCGAATCCCCTGGAAGCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTTAGTCTCTCAAATTCAGTCCC
 CTGACCCCTTCTCTGGGACACT**ATG**TTGTTCTCCGCCCTCTGCTGGAGGTGATTTGGATCC
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA
 GCCCTTTACCCTGAGTGTGGAACAATGCCAGTCGCCATCGATATTCAGACAGACAGTGT
 GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCAGC
 CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACTGCACTGGGGTCAGAAAGGATC
 CCCAGGGGGTGCAGAACACCAGATCAACAGTGAAGCCACATTTCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG
 AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCTT
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGTCCCAGATTTCAATGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
 CCTTCTCTGGCTGTTTTATTTCATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTCACCTCAGCACAGCCACGACTGAGGCAT**TAA**ATTCTCTCTCAGATACCA
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCTTCCCTGGACATCTCTTAGAGAG
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTGTGTTTAGTTGCAGGG
 GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTTCCTTAGATA
 TACTGCGGGATCTCTCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGTATCAATA
 TATTGGAAATTAAAGTTTCTGACTTT

FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQ¹DHWPASYPECGNNAS²PIDIQ³TDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSPGGSEHQ
INSEATFAELHIVHYDS⁴SDSYDSLSEAAERPQGLAVLGILIEVGETKNIA⁵YEHL⁶SHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT⁷L
FSTEEEPSKLLVQNYRALQPLNQRMV⁸FASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKS⁹VVFTSAQATTEA

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

Figure 1 illustrates the development of the human embryo from fertilization to the end of the eighth week. The diagrams are arranged vertically and labeled with numbers 1 through 12. Each diagram shows a different stage of growth, with labels indicating the corresponding week of development. The diagrams show the progression from a single cell to a complex, multi-layered structure with distinct head, trunk, and tail regions.

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGFDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPVFVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

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FIGURE 245

GGAGAGAGGCGCGCGGGTGA~~AA~~AGGCGCATTGATGCAGCCTGCGGCGGCCCTCGGAGCGCGGCG
 GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCTCCGCCCTCCAGCTCCGCGCTGCCCCG
 GCAGCCGGGAGCC~~ATG~~CGACCCAGGGCCCCGCCCTCCCCGCAGCGGCTCCGCGGCCCTCC
 TGTGCTCCTGCTGCTGCAGTGCCCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
 GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAG
 GAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTGACATTTACAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
 TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTGAGCGTTGGTATTTACATTCT
 AATGGAGCTGAATGTTTCAAGACCTCTTCCATTGAAGCTATAATTTATTTGGACCAAGGAAG
 CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAAGATTACCAAAA
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA~~TA~~
~~AA~~TGCTTTAATTTTCATTTGTACCTCTTTTTTTTATTATGCCTTGAATGGTTCACTTAAAT
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAGCAAAGCTAAATATGTTTACAGA
 CCAAAGTGATTTACACTGTTTTTAAATCTAGCATTATTCAATTTTGCTTCAATCAAAGT
 GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
 TAATTTGGAATATTGTTGTGGTCTTTTGTCTTTTCTCTTAGTATAGCATTTTTAAAAAATA
 TAAAAGCTACCAATCTTTGTACAATTGTAAATGTTAAGAATTTTTTTTATATCTGTAAAT
 AAAAAATTATTTCCAACA

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKQKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIYLDQGSPEMN
STINIHRSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217